

GenCore version 5.1.4\_p5\_4578  
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OM protein - protein search, using sw model

Run on: May 6, 2003, 10:17:10 ; Search time 35 Seconds  
(without alignments)  
22.843 Million cell updates/sec

Title: US-09-555-115a-66

Perfect score: 43

Sequence: 1 CCGKTC 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /SID2/gcgdata/geneseq-emb1/AA1980.DAT:\*
- 2: /SID2/gcgdata/geneseq-emb1/AA1981.DAT:\*
- 3: /SID2/gcgdata/geneseq-emb1/AA1982.DAT:\*
- 4: /SID2/gcgdata/geneseq-emb1/AA1983.DAT:\*
- 5: /SID2/gcgdata/geneseq-emb1/AA1984.DAT:\*
- 6: /SID2/gcgdata/geneseq-emb1/AA1985.DAT:\*
- 7: /SID2/gcgdata/geneseq-emb1/AA1986.DAT:\*
- 8: /SID2/gcgdata/geneseq-emb1/AA1987.DAT:\*
- 9: /SID2/gcgdata/geneseq-emb1/AA1988.DAT:\*
- 10: /SID2/gcgdata/geneseq-emb1/AA1990.DAT:\*
- 11: /SID2/gcgdata/geneseq-emb1/AA1991.DAT:\*
- 12: /SID2/gcgdata/geneseq-emb1/AA1992.DAT:\*
- 13: /SID2/gcgdata/geneseq-emb1/AA1993.DAT:\*
- 14: /SID2/gcgdata/geneseq-emb1/AA1994.DAT:\*
- 15: /SID2/gcgdata/geneseq-emb1/AA1995.DAT:\*
- 16: /SID2/gcgdata/geneseq-emb1/AA1996.DAT:\*
- 17: /SID2/gcgdata/geneseq-emb1/AA1997.DAT:\*
- 18: /SID2/gcgdata/geneseq-emb1/AA1998.DAT:\*
- 19: /SID2/gcgdata/geneseq-emb1/AA1999.DAT:\*
- 20: /SID2/gcgdata/geneseq-emb1/AA2000.DAT:\*
- 21: /SID2/gcgdata/geneseq-emb1/AA2001.DAT:\*
- 22: /SID2/gcgdata/geneseq-emb1/AA2002.DAT:\*
- 23: /SID2/gcgdata/geneseq-emb1/AA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	43	100.0	6	20	AAV06261
2	39	90.7	779	22	ABR66318
3	38	88.4	33	23	ABR09028
4	38	88.4	232	21	AAV09023
5	37	86.0	27	23	ABR6741
6	37	86.0	27	23	ABR6846
7	37	86.0	33	23	ABR09013
8	37	86.0	33	23	ABR09014
9	37	86.0	33	23	ABR09015
10	37	86.0	33	23	ABR09016

11	37	86.0	33	23	ABR09017	Imperatoxin linear
12	37	86.0	33	23	ABR09018	Imperatoxin linear
13	37	86.0	33	23	ABR09019	Imperatoxin linear
14	37	86.0	33	23	ABR09020	Imperatoxin linear
15	37	86.0	33	23	ABR09021	Imperatoxin linear
16	37	86.0	33	23	ABR09022	Imperatoxin linear
17	37	86.0	33	23	ABR09023	Imperatoxin linear
18	37	86.0	33	23	ABR09024	Imperatoxin linear
19	37	86.0	33	23	ABR09025	Imperatoxin linear
20	37	86.0	33	23	ABR09026	Imperatoxin linear
21	37	86.0	33	23	ABR09027	Imperatoxin linear
22	37	86.0	33	23	ABR09028	Imperatoxin linear
23	37	86.0	33	23	ABR09029	Imperatoxin linear
24	37	86.0	33	23	ABR09030	Imperatoxin linear
25	37	86.0	33	23	ABR09031	Imperatoxin linear
26	37	86.0	33	23	ABR09032	Imperatoxin linear
27	37	86.0	33	23	ABR09033	Imperatoxin linear
28	37	86.0	33	23	ABR09034	Imperatoxin linear
29	37	86.0	33	23	ABR09035	Imperatoxin linear
30	37	86.0	33	23	ABR09036	Imperatoxin linear
31	37	86.0	33	23	ABR09037	Imperatoxin linear
32	37	86.0	33	23	ABR09038	Imperatoxin linear
33	37	86.0	33	23	ABR09039	Imperatoxin linear
34	37	86.0	33	23	ABR09040	Imperatoxin linear
35	37	86.0	33	23	ABR09041	Imperatoxin linear
36	37	86.0	33	23	ABR09042	Imperatoxin linear
37	37	86.0	33	23	ABR09043	Imperatoxin linear
38	37	86.0	33	23	ABR09044	Imperatoxin linear
39	37	86.0	33	23	ABR09045	Imperatoxin linear
40	37	86.0	33	23	ABR09046	Imperatoxin linear
41	37	86.0	33	23	ABR09047	Imperatoxin linear
42	37	86.0	33	23	ABR09048	Imperatoxin linear
43	37	86.0	33	23	ABR09049	Imperatoxin linear
44	37	86.0	33	23	ABR09050	Imperatoxin linear
45	37	86.0	33	23	ABR09051	Imperatoxin linear

#### ALIGNMENTS

RESULT 1

ID AAV06261 standard; Peptide: 6 AA.

XX AAV06261;

XX 23-AUG-1999 (first entry)

XX Staphylococcal enterotoxin mutant SEC1-12 loop deletion region.

XX Enterotoxin; SEC1; toxin; disulfide loop; protein engineering;

XX mutant.

XX Staphylococcus aureus.

XX Synthetic.

XX WO927889-A2.

XX 10-JUN-1999.

XX 01-DEC-1998; 98WO-US25107.

XX 02-DEC-1997; 97US-0067357.

XX (IDAH-) IDAHO RES FOUND INC.

XX Bohach GI;

XX WPI; 1999-358008/30.

XX N-PSDB; AAX58887.

XX Non-toxic modified staphylococcal enterotoxins

PS Claim 16; Page 23; 25pp; English.

CC This sequence represents the mutated disulfide loop region of  
CC Staphylococcus aureus group C enterotoxin SEC1 deletion mutant  
CC SEC1-12. Amino acids 95-106 in the disulfide loop region of  
CC native SEC1 (see AA06249) are deleted in SEC1-12, and the residue  
CC corresponding to native Tyr-94 is changed to Cys. The invention  
CC relates to pyrogenic toxins, such as staphylococcal enterotoxins,  
CC that are modified in the disulfide loop. Typically, the  
CC modification involves deletions within the disulfide loop region  
CC of SEC1 (see AA06259-61). The modified toxins retain useful  
CC biological properties, such as the ability to induce cytokine  
CC production, but have substantially reduced toxicity compared to  
CC the corresponding unmodified native toxin. Emetic response  
CC inducing activity and fever inducing activity are typically  
CC decreased by at least about 100-fold, while ID50 (in Dutch Belted  
CC rabbits) is at least 100-fold higher than the native toxin.

XX Sequence 6 AA;

Query Match 100.0%; Score 43; DB 20; Length 6;  
Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCGKTC 6  
| | | | |  
DB 1 CCGKTC 6

RESULT 2  
ID ABB66318 standard; Protein; 779 AA.

XX ABB66318;  
XX 26-MAR-2002 (first entry)

DE Drosophila melanogaster polypeptide SEQ ID NO 25746.  
XX  
XX Drosophila: developmental biology; cell signalling; insecticide;  
KM Pharmaceutical.  
XX  
XX Drosophila melanogaster.  
OS  
XX WO200171042-A2.  
PN  
XX 27-SEP-2001.  
PD  
XX 23-MAR-2001; 2001WO-US09231.  
PF  
XX 23-MAR-2000; 2000US-191637P.  
PR 11-JUL-2000; 2000US-0614150.  
XX  
XX (PEKE ) PE CORP NY.  
PA  
XX Venter JC, Adams M, Li PWD, Myers EW;  
PI  
XX WPI; 2001-656860/75.  
DR N-PSDB; ABL10421.  
DR  
XX New isolated nucleic acid detection reagent for detecting 1000 or more  
PT genes from Drosophila and for elucidating cell signalling and cell-cell  
PT interactions -  
XX  
XX Disclosure; SEQ ID NO 25746; 21pp + Sequence Listing; English.

CC The invention relates to an isolated nucleic acid detection reagent  
CC capable of detecting 1000 or more genes from Drosophila. The invention is  
CC useful in developmental biology and in elucidating cell signalling and  
CC cell-cell interactions in higher eukaryotes for the development of  
CC insecticides, therapeutics and pharmaceutical drugs. The invention  
CC discloses genomic DNA sequences (ABL16176-ABL30513), expressed DNA  
CC sequences (ABL01840-ABL16175) and the encoded proteins

CC (ABB57737-ABB72072).  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 779 AA;

Query Match 90.7%; Score 39; DB 22; Length 779;  
Best Local Similarity 83.3%; Pred. No. 5.3e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCGKTC 6  
| | | | |  
DB 340 CCGKTC 345

RESULT 3  
ID ABB09028 standard; peptide; 33 AA.

XX ABB09028;  
XX 03-MAY-2002 (first entry)

DE Imperatoxin linear peptide #16.  
XX  
XX Imperatoxin; muscle disorder.  
KM  
XX Unidentified.  
OS  
XX KR2001070886-A.  
PN  
XX 27-JUL-2001.  
PD  
XX 18-JUN-2001; 2001KR-0034219.  
PF  
XX 18-JUN-2001; 2001KR-0034219.  
PR  
XX (ANYG-) ANYGEN CO LTD.  
PA (KMAN-) KMANJU INST SCI & TECHNOLOGY.  
XX  
XX Kim DH, Kim JI, Lee CW;  
PI  
XX WPI; 2002-081143/11.  
DR  
XX Three dimensional structure of peptide Imperatoxin and its  
PT physiologically active region and manufacturing method -  
PT  
XX Disclosure; Fig 4; 19pp; Korean.

PS  
XX This invention relates to manufacturing Imperatoxin peptides in a high  
CC yield and developing Imperatoxin in a three dimensional structure  
CC which is useful in developing medications against muscle disorders.  
CC This peptide sequence represents a linear Imperatoxin peptide.

XX Sequence 33 AA;

Query Match 88.4%; Score 38; DB 23; Length 33;  
Best Local Similarity 83.3%; Pred. No. 73;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CCGKTC 6  
| | | | |  
DB 16 CCGKTC 21

RESULT 4  
ID AAY50923 standard; Protein; 232 AA.

XX AAY50923;  
XX 10-MAR-2000 (first entry)

XX DE Human fetal brain cDNA clone vc10\_1 derived protein.  
 XX KM Human: secreted protein; treatment; nutritional activity; cytokine;  
 KM cell proliferation; cell differentiation; hematopoiesis regulation;  
 KM tissue growth; activin; inhibin; chemotactic; chemokine; hemostatic;  
 KM thrombolytic; anti-inflammatory; invasion suppressor; tumor inhibition;  
 KM gene therapy.  
 OS Homo sapiens.  
 XX PN W09955721-A1.  
 PD 04-NOV-1999.  
 XX PF 23-APR-1999; 99MO-US08504.  
 XX PF 24-APR-1998; 98US-0082904.  
 PR 11-JUN-1998; 98US-0088994.  
 PR 12-JUN-1998; 98US-0089278.  
 PR 02-JUL-1998; 98US-0091647.  
 PR 24-AUG-1998; 98US-0097639.  
 PR 22-APR-1999; 99US-0097639.  
 XX (ALPH-) ALPHAGENE INC.  
 XX PI Valenzuela D, Yuan O, Hoffman H, Hall J, Raplejo P;  
 XX WPI: 2000-052801/04.  
 DR N-PSDB; AAZ43730.  
 XX PT New polynucleotides encoding secreted human proteins, derived from  
 PT human fetal brain, adult skin, adult brain, adult heart, adult thymus  
 PT and adult aorta cDNA libraries.  
 XX Claim 37a; Page 235-236; 282pp; English.  
 PS This invention describes novel human secreted proteins which are encoded  
 CC by polynucleotides obtained from fetal brain, adult skin, adult brain,  
 CC adult heart, adult thymus and adult aorta cDNA libraries. The  
 CC polynucleotides and proteins are predicted to have biological activities  
 CC which would make them suitable for treating, preventing or ameliorating  
 CC medical conditions in humans and animals, although no supporting data  
 CC is given. Suggested activities include nutritional activity, cytokine  
 CC and cell proliferation/differentiation activity, immune stimulating  
 CC (e.g. as vaccines) or suppressing activity, hematopoiesis regulating  
 CC activity, tissue growth activity, activin/inhibin activity,  
 CC chemotactic/chemokine activity, hemostatic and thrombolytic activity,  
 CC receptor/ligand activity, anti-inflammatory activity, cadherin/tumor  
 CC invasion suppressor activity, and tumor inhibition activity.  
 CC polynucleotides are also stated to be useful for gene therapy.  
 CC AA55905-Y50947 represent the secreted proteins described in the method  
 CC of the invention which are encoded by the polynucleotides represented in  
 CC AAZ4377-243808.  
 XX Sequence 232 AA;  
 SQ  
 Query Match 88.4%; Score 38; DB 21; Length 232;  
 Best Local Similarity 83.3%; Pred. No. 3e+02;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 CCGATC 6  
 11111  
 Db 70 CCGGTC 75  
 RESULT 5  
 ABB96741  
 ID ABB96741 standard; Peptide: 27 AA.  
 XX ABB96741:  
 AC  
 XX 12-JUL-2002 (first entry)

XX DE Omega-conopeptide E6.2 generic toxin sequence.  
 XX KM Omega-conopeptide; analgesic; anticonvulsant; vasotropic; cardiant;  
 KM neuroprotective; cerebroprotective; cardiovascular; antiinflammatory;  
 KM antinigraine; antidiabetic; tranquiliser; vulnary; antipsychotic;  
 KM antilytic; neuroleptic; voltage gated ion channel; seizure; epilepsy;  
 KM neurological disorder; neurotoxic injury; hypoxia; anoxia; ischaemia;  
 KM stroke; cerebrovascular accident; brain trauma; spinal chord trauma;  
 KM drowning; suffocation; perinatal asphyxia; hypoglycaemic event; pain;  
 KM migraine; inflammation; cardiovascular disorder; psychiatric disorder;  
 KM psychosis; anxiety; schizophrenia.  
 XX Conus ermineus.  
 OS  
 XX FH Key location/Qualifiers  
 FT MISC-difference 1 /label- OTHER  
 FT /note- OTHER is Pro or Hydroxy Pro"  
 FT MISC-difference 4 /label- OTHER  
 FT /note- OTHER is Pro or Hydroxy Pro"  
 FT MISC-difference 11 /label- OTHER  
 FT /note- OTHER is Pro or Hydroxy Pro"  
 FT MISC-difference 27 /label- OTHER  
 FT /note- OTHER is Pro or Hydroxy Pro"  
 XX W0200207675-A2.  
 XX 31-JAN-2002.  
 XX 23-JUL-2001; 2001WO-US23041.  
 XX 21-JUL-2000; 2000US-219616P.  
 XX 05-FEB-2001; 2001US-265888P.  
 XX (UTAH ) UNIV UTAH RES FOUND.  
 XX (COGN-) COGNETIX INC.  
 XX Olivera BM, McIntosh JM, Watkins M, Garrett JE, Shon K;  
 XX Jacobsen R, Jones RM, Cartier GE;  
 XX WPI: 2002-257318/30.  
 XX New omega-conopeptides useful for treating disorders associated with  
 PT voltage gated ion channels e.g. pain, inflammation, neurological or  
 PT cardiovascular disorders -  
 PS Example 2; Page 42; 195pp; English.  
 XX The invention relates to isolated omega-conopeptides, nucleic acid  
 CC sequences encoding them, and propeptide sequences. The activity of  
 CC the peptides of the invention may be described as, analgesic,  
 CC anticonvulsant, vasotropic, cardiant, neuroprotective, cerebroprotective,  
 CC cardiovascular, antiinflammatory, antinigraine, antidiabetic,  
 CC tranquiliser, vulnary, antipsychotic, antilytic and neuroleptic.  
 CC peptides of the invention act by modulating the activity of voltage gated  
 CC ion channels. They may be used for treating or preventing disorders  
 CC associated with voltage gated ion channels such as neurological  
 CC disorders, e.g. seizure (associated with epilepsy), neurotoxic injury  
 CC associated with conditions of hypoxia, anoxia, ischaemia, stroke,  
 CC cerebrovascular accident, brain or spinal chord trauma, stroke,  
 CC suffocation, perinatal asphyxia or hypoglycaemic events; pain e.g.  
 CC migraine; inflammation or cardiovascular disorders. They may also be used  
 CC for treating psychiatric disorders e.g. psychosis, anxiety or  
 CC schizophrenia. The analgesic agents of the invention show diminished side  
 CC effects and toxicity, and are non-addictive. The sequences given in  
 CC records ABB96698-ABB96806 represent omega-conopeptide generic toxin  
 CC sequences.  
 XX Sequence 27 AA;  
 SQ

Query Match 86.0%; Score 37; DB 23; Length 27;  
 Best Local Similarity 83.3%; Pred. No. 86;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 CCGKTC 6  
 11111  
 DB 16 CCKKTC 21

## RESULT 6

ABR96846  
 ID ABR96846 standard; Peptide; 27 AA.

AC ABR96846;  
 XX

DT 12-JUL-2002 (first entry)  
 XX

DE Omega-conopeptide E6.2 toxin sequence.  
 XX

XX Omega-conopeptide; analgesic; anticonvulsant; vasotropic; cardiant;  
 KW neuroprotective; cerebroprotective; cardiovascular; antiinflammatory;  
 KW antidiarrhoeal; antidiabetic; tranquiliser; vulnerary; antipsychotic;  
 KW anxiolytic; neuroleptic; voltage gated ion channel; seizure; epilepsy;  
 KW neurological disorder; neurotoxic injury; hypoxia; anoxia; ischaemia;  
 KW stroke; cerebrovascular accident; brain trauma; spinal chord trauma;  
 KW drowning; suffocation; perinatal asphyxia; hypoglycaemic event; pain;  
 KW migraine; inflammation; cardiovascular disorder; psychiatric disorder;  
 KW psychosis; anxiety; schizophrenia.

XX Conus ermineus.  
 XX

XX WO200207675-A2.  
 XX

PD 31-JAN-2002.  
 XX

PF 23-JUL-2001; 2001WO-US23041.  
 XX

PR 21-JUL-2000; 2000US-219616P.  
 XX

PR 05-FEB-2001; 2001US-265888P.  
 XX

XX (UTAH) UNIV UTAH RES FOUND.  
 PA (COGN-) COGNETIX INC.

XX Olivera BM, McIntosh JM, Watkins M, Garrett JE, Shon K;  
 PI Jacobsen R, Jones RM, Cartier GE;

XX WPI; 2002-257318/30.  
 DR

XX New omega-conopeptides useful for treating disorders associated with  
 PT voltage gated ion channels e.g. pain, inflammation, neurological or  
 PT cardiovascular disorders -

PS Claim 1(a); Page 71; 195pp; English.  
 XX

XX The invention relates to isolated omega-conopeptides, nucleic acid  
 CC sequences encoding them, and propeptide sequences. The activity of  
 CC the peptides of the invention may be described as, analgesic,  
 CC anticonvulsant, vasotropic, cardiant, neuroprotective, cerebroprotective,  
 CC cardiovascular, antiinflammatory, antidiarrhoeal, antidiabetic,  
 CC tranquiliser, vulnerary, antipsychotic, anxiolytic and neuroleptic.  
 CC Peptides of the invention act by modulating the activity of voltage gated  
 CC ion channels. They may be used for treating or preventing disorders  
 CC associated with voltage gated ion channels such as neurological  
 CC disorders, e.g. seizure (associated with epilepsy), neurotoxic injury  
 CC associated with conditions of hypoxia, anoxia, ischaemia, stroke,  
 CC cerebrovascular accident, brain or spinal chord trauma, drowning,  
 CC suffocation, perinatal asphyxia or hypoglycaemic events; pain e.g.  
 CC migraine; inflammation or cardiovascular disorders. They may also be used  
 CC for treating psychiatric disorders e.g. psychosis, anxiety or  
 CC schizophrenia. The analgesic agents of the invention show diminished side  
 CC effects and toxicity, and are non-addictive. The sequences given in  
 CC records ABR96807-ABR96905 represent omega-conopeptide toxin sequences.

XX SQ Sequence 27 AA;  
 SQ

Query Match 86.0%; Score 37; DB 23; Length 27;  
 Best Local Similarity 83.3%; Pred. No. 86;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 CCGKTC 6  
 11111  
 DB 16 CCKKTC 21

XX  
 DB 16 CCKKTC 21

## RESULT 7

ABR09013  
 ID ABR09013 standard; peptide; 33 AA.

XX ABR09013;  
 XX

AC ABR09013;  
 XX

DT 03-MAY-2002 (first entry)  
 XX

DE Imperatoxin linear peptide #1.  
 XX

XX Imperatoxin; muscle disorder.  
 KW

XX Unidentified.  
 OS

XX KR2001070886-A.  
 PN

XX 27-JUL-2001.  
 PD

XX 18-JUN-2001; 2001KR-0034219.  
 PF

XX 18-JUN-2001; 2001KR-0034219.  
 PR

XX (ANYG-) ANYGEN CO LTD.  
 PA (KMAN-) KWANGJU INST SCI & TECHNOLOGY.

XX Kim DH, Kim JI, Lee CW;  
 PI

XX WPI; 2002-081143/11.  
 DR

XX Three dimensional structure of peptide imperatoxin and its  
 PT physiologically active region and manufacturing method -

XX Disclosure; Fig 4; 19pp; Korean.  
 PS

XX This invention relates to manufacturing imperatoxin peptides in a high  
 CC yield and developing imperatoxin in a three dimensional structure  
 CC which is useful in developing medications against muscle disorders.  
 CC This peptide sequence represents a linear imperatoxin peptide.

XX Sequence 33 AA;  
 SQ

Query Match 86.0%; Score 37; DB 23; Length 33;  
 Best Local Similarity 83.3%; Pred. No. 99;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCGKTC 6  
 11111  
 DB 16 CCGKTC 21

XX  
 DB 16 CCGKTC 21

## RESULT 8

ABR09014  
 ID ABR09014 standard; peptide; 33 AA.

XX ABR09014;  
 XX

AC ABR09014;  
 XX

DT 03-MAY-2002 (first entry)  
 XX

DE Imperatoxin linear peptide #2.  
 KW

XX Imperatoxin; muscle disorder.  
 KW

XX Unidentified.  
OS  
XX KR2001070886-A.  
PN  
XX  
PD 27-JUL-2001.  
XX  
PF 18-JUN-2001; 2001KR-0034219.  
XX  
PR 18-JUN-2001; 2001KR-0034219.  
XX  
PA (ANYG-) ANYGEN CO LTD.  
PI (KMAN-) KWANGJU INST SCI & TECHNOLOGY.  
XX  
PI Kim DH, Kim JI, Lee CW;  
XX  
DR WPI; 2002-081143/11.  
XX  
PT Three dimensional structure of peptide imperatoxin and its  
physiologically active region and manufacturing method -  
XX  
PS Disclosure; Fig 4; 19pp; Korean.  
XX  
CC This invention relates to manufacturing imperatoxin peptides in a high  
yield and developing imperatoxin in a three dimensional structure  
CC which is useful in developing medications against muscle disorders.  
CC This peptide sequence represents a linear imperatoxin peptide.  
XX  
SQ Sequence 33 AA;  
SO  
Query Match 86.0%; Score 37; DB 23; Length 33;  
Best Local Similarity 83.3%; Pred. No. 99;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 1 CCGKTC 6  
DB 16 CCGKKC 21  
RESULT 9  
ABB09015  
ID ABB09015 standard; peptide; 33 AA.  
XX  
AC ABB09015;  
XX  
DT 03-MAY-2002 (first entry)  
XX  
DE Imperatoxin linear peptide #3.  
XX  
KW Imperatoxin; muscle disorder.  
XX  
OS Unidentified.  
XX  
PN KR2001070886-A.  
XX  
PD 27-JUL-2001.  
XX  
PF 18-JUN-2001; 2001KR-0034219.  
XX  
PR 18-JUN-2001; 2001KR-0034219.  
XX  
PA (ANYG-) ANYGEN CO LTD.  
PI (KMAN-) KWANGJU INST SCI & TECHNOLOGY.  
XX  
PI Kim DH, Kim JI, Lee CW;  
XX  
DR WPI; 2002-081143/11.  
XX  
PT Three dimensional structure of peptide imperatoxin and its  
physiologically active region and manufacturing method -  
XX  
PS Disclosure; Fig 4; 19pp; Korean.  
XX

CC This invention relates to manufacturing imperatoxin peptides in a high  
yield and developing imperatoxin in a three dimensional structure  
CC which is useful in developing medications against muscle disorders.  
CC This peptide sequence represents a linear imperatoxin peptide.  
XX  
SQ Sequence 33 AA;  
SO  
Query Match 86.0%; Score 37; DB 23; Length 33;  
Best Local Similarity 83.3%; Pred. No. 99;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 1 CCGKTC 6  
DB 16 CCGKKC 21  
RESULT 10  
ABB09016  
ID ABB09016 standard; peptide; 33 AA.  
XX  
AC ABB09016;  
XX  
DT 03-MAY-2002 (first entry)  
XX  
DE Imperatoxin linear peptide #4.  
XX  
KW Imperatoxin; muscle disorder.  
XX  
OS Unidentified.  
XX  
PN KR2001070886-A.  
XX  
PD 27-JUL-2001.  
XX  
PF 18-JUN-2001; 2001KR-0034219.  
XX  
PR 18-JUN-2001; 2001KR-0034219.  
XX  
PA (ANYG-) ANYGEN CO LTD.  
PI (KMAN-) KWANGJU INST SCI & TECHNOLOGY.  
XX  
PI Kim DH, Kim JI, Lee CW;  
XX  
DR WPI; 2002-081143/11.  
XX  
DT Three dimensional structure of peptide imperatoxin and its  
physiologically active region and manufacturing method -  
XX  
PS Disclosure; Fig 4; 19pp; Korean.  
XX  
OS This invention relates to manufacturing imperatoxin peptides in a high  
yield and developing imperatoxin in a three dimensional structure  
CC which is useful in developing medications against muscle disorders.  
CC This peptide sequence represents a linear imperatoxin peptide.  
XX  
SQ Sequence 33 AA;  
SO  
Query Match 86.0%; Score 37; DB 23; Length 33;  
Best Local Similarity 83.3%; Pred. No. 99;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 1 CCGKTC 6  
DB 16 CCGKKC 21  
RESULT 11  
ABB09017  
ID ABB09017 standard; peptide; 33 AA.  
XX  
AC ABB09017;  
XX  
DT 03-MAY-2002 (first entry)  
XX

XX Imperatoxin linear peptide #5.  
DE  
XX Imperatoxin; muscle disorder.  
KW  
XX Unidentified.  
OS  
XX KR2001070886-A.  
PN  
XX  
XX 27-JUL-2001.  
PD  
XX  
XX 18-JUN-2001; 2001KR-0034219.  
PF  
XX  
XX 18-JUN-2001; 2001KR-0034219.  
PR  
XX  
XX (ANYG-) ANYGEN CO LTD.  
PA (KWAN-) KWANGJU INST SCI & TECHNOLOGY.  
XX  
XX Kim DH, Kim JI, Lee CW;  
PI  
XX WPI: 2002-081143/11.  
DR  
XX  
PT Three dimensional structure of peptide Imperatoxin and its physiologically active region and manufacturing method -

PS Disclosure: Fig 4; 19pp: Korean.  
XX  
XX This invention relates to manufacturing Imperatoxin peptides in a high yield and developing Imperatoxin in a three dimensional structure which is useful in developing medications against muscle disorders.  
CC  
XX This peptide sequence represents a linear Imperatoxin peptide.  
CC  
XX  
SQ Sequence 33 AA;  
Query Match 86.0%; Score 37; DB 23; Length 33;  
Best Local Similarity 83.3%; Pred. No. 99;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CCGKTC 6  
||| |  
DB 16 CCGKTC 21

RESULT 12  
ABB09018  
ID ABB09018 standard; peptide: 33 AA.  
XX  
XX ABB09018;  
AC  
XX  
XX 03-MAY-2002 (first entry)  
DT  
XX  
XX Imperatoxin linear peptide #6.  
DE  
XX  
XX Imperatoxin; muscle disorder.  
KW  
XX  
XX Unidentified.  
OS  
XX KR2001070886-A.  
PN  
XX  
XX 27-JUL-2001.  
PD  
XX  
XX 18-JUN-2001; 2001KR-0034219.  
PF  
XX  
XX 18-JUN-2001; 2001KR-0034219.  
PR  
XX  
XX (ANYG-) ANYGEN CO LTD.  
PA (KWAN-) KWANGJU INST SCI & TECHNOLOGY.  
XX  
XX Kim DH, Kim JI, Lee CW;  
PI  
XX WPI: 2002-081143/11.  
DR  
XX  
PT Three dimensional structure of peptide Imperatoxin and its

PT physiologically active region and manufacturing method -  
XX  
XX Disclosure; Fig 4; 19pp: Korean.  
PS  
XX  
XX This invention relates to manufacturing Imperatoxin peptides in a high yield and developing Imperatoxin in a three dimensional structure which is useful in developing medications against muscle disorders.  
CC  
XX This peptide sequence represents a linear Imperatoxin peptide.  
CC  
XX  
SQ Sequence 33 AA;  
Query Match 86.0%; Score 37; DB 23; Length 33;  
Best Local Similarity 83.3%; Pred. No. 99;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CCGKTC 6  
||| |  
DB 16 CCGKTC 21

RESULT 13  
ABB09019  
ID ABB09019 standard; peptide: 33 AA.  
XX  
XX ABB09019;  
AC  
XX  
XX 03-MAY-2002 (first entry)  
DT  
XX  
XX Imperatoxin linear peptide #7.  
DE  
XX  
XX Imperatoxin; muscle disorder.  
KW  
XX  
XX Unidentified.  
OS  
XX KR2001070886-A.  
PN  
XX  
XX 27-JUL-2001.  
PD  
XX  
XX 18-JUN-2001; 2001KR-0034219.  
PF  
XX  
XX 18-JUN-2001; 2001KR-0034219.  
PR  
XX  
XX (ANYG-) ANYGEN CO LTD.  
PA (KWAN-) KWANGJU INST SCI & TECHNOLOGY.  
XX  
XX Kim DH, Kim JI, Lee CW;  
PI  
XX WPI: 2002-081143/11.  
DR  
XX  
XX Three dimensional structure of peptide Imperatoxin and its physiologically active region and manufacturing method -

PS Disclosure: Fig 4; 19pp: Korean.  
XX  
XX This invention relates to manufacturing Imperatoxin peptides in a high yield and developing Imperatoxin in a three dimensional structure which is useful in developing medications against muscle disorders.  
CC  
XX This peptide sequence represents a linear Imperatoxin peptide.  
CC  
XX  
SQ Sequence 33 AA;  
Query Match 86.0%; Score 37; DB 23; Length 33;  
Best Local Similarity 83.3%; Pred. No. 99;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CCGKTC 6  
||| |  
DB 16 CCGKTC 21

RESULT 14  
ABB09020  
ID ABB09020 standard; peptide: 33 AA.

XX ABB09020;  
AC 03-MAY-2002 (first entry)  
DT Imperatoxin linear peptide #8.  
XX Imperatoxin; muscle disorder.  
KW Unidentified.  
XX KR2001070886-A.  
XX 27-JUL-2001.  
PD 18-JUN-2001; 2001KR-0034219.  
PF 18-JUN-2001; 2001KR-0034219.  
XX (ANYG-) ANYGEN CO LTD.  
PA (KWAN-) KWANGJU INST SCI & TECHNOLOGY.  
XX Kim DH, Kim JI, Lee CW;  
PI WPI; 2002-081143/11.  
DR Three dimensional structure of peptide imperatoxin and its  
XX physiologically active region and manufacturing method -  
XX PS Disclosure; Fig 4; 19pp; Korean.  
XX CC This invention relates to manufacturing imperatoxin peptides in a high  
CC yield and developing imperatoxin in a three dimensional structure  
CC which is useful in developing medications against muscle disorders.  
XX CC This peptide sequence represents a linear imperatoxin peptide.  
SQ Sequence 33 AA;  
Query Match 86.0%; Score 37; DB 23; Length 33;  
Best Local Similarity 83.3%; Pred. No. 99;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 CCGKTC 6  
DB 16 CCGKCC 21  
RESULT 15  
ABB09021  
ID ABB09021 standard; peptide; 33 AA.  
XX ABB09021;  
AC 03-MAY-2002 (first entry)  
DT Imperatoxin linear peptide #9.  
XX Imperatoxin; muscle disorder.  
KW Unidentified.  
XX KR2001070886-A.  
XX 27-JUL-2001.  
PD 18-JUN-2001; 2001KR-0034219.  
PF 18-JUN-2001; 2001KR-0034219.  
XX (ANYG-) ANYGEN CO LTD.  
PA (KWAN-) KWANGJU INST SCI & TECHNOLOGY.  
XX Kim DH, Kim JI, Lee CW;  
PI

XX WPI; 2002-081143/11.  
DR Three dimensional structure of peptide imperatoxin and its  
XX physiologically active region and manufacturing method -  
XX PS Disclosure; Fig 4; 19pp; Korean.  
XX CC This invention relates to manufacturing imperatoxin peptides in a high  
CC yield and developing imperatoxin in a three dimensional structure  
CC which is useful in developing medications against muscle disorders.  
XX CC This peptide sequence represents a linear imperatoxin peptide.  
SQ Sequence 33 AA;  
Query Match 86.0%; Score 37; DB 23; Length 33;  
Best Local Similarity 83.3%; Pred. No. 99;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 CCGKTC 6  
DB 16 CCGKCC 21

Search completed: May 6, 2003, 10:29:11  
Job time : 37 secs

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## OM protein - protein search, using sw model

Run on: May 6, 2003, 10:28:55 ; Search time 14 Seconds  
(without alignments)  
12.610 Million cell updates/sec

Title: US-09-555-115A-66  
Perfect score: 43  
Sequence: 1 CCGKTC 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues  
Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
1: /cgn2\_6/ptodata/1/1aa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/1/1aa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/PCRTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/Backfills1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	37	86.0	1345	2	US-08-977-767-3
2	37	86.0	1400	4	US-08-630-915A-37
3	37	86.0	1417	4	US-08-900-230-3
4	37	86.0	1917	4	US-09-627-650B-5
5	37	86.0	1917	4	US-09-436-063C-5
6	36	83.7	57	4	US-08-900-230-59
7	36	83.7	2088	4	US-09-548-372D-13
8	36	83.7	2088	4	US-09-548-367D-13
9	35	81.4	24	4	US-09-201-227A-34
10	35	81.4	38	2	US-08-902-516-47
11	35	81.4	111	4	US-09-201-227A-39
12	35	81.4	2211	4	US-09-738-884-1
13	34	79.1	124	4	US-09-201-227A-37
14	34	79.1	154	4	US-09-201-227A-4
15	34	79.1	154	4	US-09-201-227A-18
16	34	79.1	193	3	US-08-842-976-3
17	34	79.1	193	3	US-08-842-976-4
18	34	79.1	193	3	US-09-213-397-3
19	34	79.1	193	3	US-09-213-397-4
20	34	79.1	193	3	US-09-416-489-3
21	34	79.1	193	3	US-09-416-489-4
22	34	79.1	197	1	US-07-914-284A-8
23	34	79.1	198	4	US-08-842-306B-2
24	34	79.1	198	4	US-08-838-973B-2
25	34	79.1	198	4	US-08-771-212A-2
26	34	79.1	202	2	US-08-948-616-11
27	34	79.1	202	2	US-09-193-510-11

28	34	79.1	202	4	US-09-368-402-11	Sequence 11, Appl
29	34	79.1	207	4	US-09-415-522-2	Sequence 2, Appl
30	33	76.7	26	4	US-09-227-357-579	Sequence 579, Appl
31	33	76.7	30	2	US-08-753-829A-8	Sequence 8, Appl
32	33	76.7	425	1	US-08-414-926A-15	Sequence 15, Appl
33	33	76.7	425	2	US-08-926-922-15	Sequence 15, Appl
34	33	76.7	425	3	US-09-253-682-15	Sequence 15, Appl
35	33	76.7	425	4	US-09-527-657-15	Sequence 15, Appl
36	33	76.7	2296	2	US-08-286-819A-27	Sequence 27, Appl
37	33	76.7	2296	3	US-08-980-357-27	Sequence 27, Appl
38	32	74.4	23	4	US-08-900-230-23	Sequence 23, Appl
39	32	74.4	197	2	US-08-855-261A-1	Sequence 1, Appl
40	32	74.4	197	4	US-09-227-224-1	Sequence 1, Appl
41	32	74.4	198	4	US-09-227-357-232	Sequence 232, App
42	32	74.4	282	3	US-09-120-365-79	Sequence 79, Appl
43	32	74.4	282	4	US-09-515-039-79	Sequence 79, Appl
44	32	74.4	339	1	US-08-208-007A-11	Sequence 11, Appl
45	32	74.4	339	1	US-08-330-121B-7	Sequence 7, Appl

## ALIGNMENTS

RESULT 1  
US-08-977-767-3  
Sequence 3, Application US/08977767  
Patent No. 5972684  
GENERAL INFORMATION:  
APPLICANT: Bandman, Olga  
APPLICANT: Yue, Henry  
APPLICANT: Greenwald, Sara  
APPLICANT: Corley, Neil C.  
TITLE OF INVENTION: CARBONIC ANHYDRASE VIII  
NUMBER OF SEQUENCES: 3  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/977,767  
FILING DATE: Herewith  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0423 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-855-0555  
TELEFAX: 650-845-4166  
TELEX:  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1345 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: Genbank  
CLONE: 1532042  
US-08-977-767-3  
Query Match 86.0%; Score 37; DB 2; Length 1345;

Best Local Similarity 83.3%; Pred. No. 4.3e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CCGKTC 6  
||| ||  
DB 820 CCGTTC 825

RESULT 2  
US-08-630-915A-37

; Sequence 37, Application US/08630915A  
; Patent No. 6309820

; GENERAL INFORMATION:

; APPLICANT: SPARKS, Andrew B.

; APPLICANT: HOFFMAN, No. 6309820h

; APPLICANT: KAY, Brian K.

; APPLICANT: FOWLES, Dana M.

; APPLICANT: MCCONNELL, Stephen J.

; TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL

; TITLE OF INVENTION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND

; NUMBER OF SEQUENCES: 227

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds LLP

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: USA

; ZIP: 10036-2711

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/630,915A

; FILING DATE: 03-APR-1996

; CLASSIFICATION: 536

; ATTORNEY/AGENT INFORMATION:

; NAME: MISTOCK, S. Leslie

; REGISTRATION NUMBER: 18,872

; REFERENCE/DOCKET NUMBER: 1101-174

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 790-9090

; TELEFAX: (212) 869-8864/9741

; TELEX: 66141 PENNIE

; INFORMATION FOR SEQ ID NO: 37:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1400 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA

; US-08-630-915A-37

Query Match 86.0%; Score 37; DB 4; Length 1400;

Best Local Similarity 83.3%; Pred. No. 4.5e+02;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CCGKTC 6  
||| ||  
DB 579 CCGTTC 584

RESULT 3  
US-08-900-230-3

; Sequence 3, Application US/08900230

; Patent No. 6329197

; GENERAL INFORMATION:

; APPLICANT: Bard, Jonathan A.

; TITLE OF INVENTION: DNA ENCODING GALANN GALR3 RECEPTORS AND

; NUMBER OF SEQUENCES: 59

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Cooper & Dunham LLP

; STREET: 1185 Avenue of The Americas

; CITY: New York

; STATE: New York

; COUNTRY: U.S.A.

; ZIP: 11036

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/900,230

; FILING DATE: 23-JUL-1997

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: White, John P.

; REGISTRATION NUMBER: 28,678

; REFERENCE/DOCKET NUMBER: 52241-C/JPW/ADM

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 212-391-0525

; TELEFAX: 212-278-0400

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1417 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE:

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; US-08-900-230-3

Query Match 86.0%; Score 37; DB 4; Length 1417;

Best Local Similarity 83.3%; Pred. No. 4.5e+02;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CCGKTC 6  
||| ||  
DB 1327 CCGTTC 1332

RESULT 4

; US-09-627-650B-5

; Sequence 5, Application US/09627650B

; Patent No. 6406872

; GENERAL INFORMATION:

; APPLICANT: Hamber, Bruce

; APPLICANT: Jorgensen, Erik

; TITLE OF INVENTION: Nematode Neuromuscular Junction GABA Receptors and

; FILE REFERENCE: 21101.000903

; CURRENT APPLICATION NUMBER: US/09/627,650B

; CURRENT FILING DATE: 2000-07-28

; PRIOR APPLICATION NUMBER: 09/436,063

; PRIOR FILING DATE: 1999-11-08

; PRIOR APPLICATION NUMBER: 60/107,727

; PRIOR FILING DATE: 1998-11-09

; NUMBER OF SEQ ID NOS: 50

; SOFTWARE: Patentin Ver. 2.1

; SEQ ID NO 5

; LENGTH: 1917

; TYPE: PRT

; ORGANISM: Caenorhabditis elegans

; US-09-627-650B-5

Query Match 86.0%; Score 37; DB 4; Length 1917;

Best Local Similarity 83.3%; Pred. No. 5.6e+02;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CCGKTC 6  
||| ||

Db 1389 CCGTTC 1394

RESULT 5

US-09-436-063C-5  
Sequence 5, Application US/09436063C  
Patent No. 6407210  
GENERAL INFORMATION:  
APPLICANT: Bamber, Bruce  
APPLICANT: Jorgensen, Erik  
TITLE OF INVENTION: Nematode Neuromuscular Junction GABA Receptors and  
FILE REFERENCE: P-1095corrected  
CURRENT APPLICATION NUMBER: US/09/436, 063C  
CURRENT FILING DATE: 1999-11-08  
PRIOR APPLICATION NUMBER: 60/107727  
PRIOR FILING DATE: 1998-11-09  
NUMBER OF SEQ ID NOS: 18  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 5  
LENGTH: 1917  
TYPE: PRT  
ORGANISM: Caenorhabditis elegans  
US-09-436-063C-5

Query Match 86.0%; Score 37; DB 4; Length 1917;  
Best Local Similarity 83.3%; Pred. No. 5.6e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCGTTC 6  
Db 1389 CCGTTC 1394

RESULT 6

US-08-900-230-59  
Sequence 59, Application US/08900230  
Patent No. 6329197  
GENERAL INFORMATION:  
APPLICANT: Baird, Jonathan A.  
TITLE OF INVENTION: DNA ENCODING GALANN GALR3 RECEPTORS AND  
TITLE OF INVENTION: USES THEREOF  
NUMBER OF SEQUENCES: 59  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper & Dunham LLP  
STREET: 1185 Avenue of The Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 11036

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/900,230  
FILING DATE: 23-JUL-1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 52241-C/JPW/ADM  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-278-0400  
TELEFAX: 212-391-0525

INFORMATION FOR SEQ ID NO: 59:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 57 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE:

HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-900-230-59

Query Match 83.7%; Score 36; DB 4; Length 57;  
Best Local Similarity 83.3%; Pred. No. 60;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCGTTC 6  
Db 48 CCGTTC 53

RESULT 7

US-09-548-372D-13  
Sequence 13, Application US/09548372D  
Patent No. 6420534  
GENERAL INFORMATION:  
APPLICANT: GURNEY ET AL.  
TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USE  
FILE REFERENCE: 29915/62801  
CURRENT APPLICATION NUMBER: US/09/548,372D  
CURRENT FILING DATE: 2000-04-12  
PRIOR APPLICATION NUMBER: US 60/155,493  
PRIOR FILING DATE: 1999-09-23  
PRIOR APPLICATION NUMBER: US 09/404,133  
PRIOR FILING DATE: 1999-09-23  
PRIOR APPLICATION NUMBER: PCT/US99/20881  
PRIOR FILING DATE: 1999-09-23  
PRIOR APPLICATION NUMBER: US 60/101,594  
PRIOR FILING DATE: 1998-09-24  
NUMBER OF SEQ ID NOS: 73  
SOFTWARE: Patentin version 3.1  
SEQ ID NO 13  
LENGTH: 2088  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-548-372D-13

Query Match 83.7%; Score 36; DB 4; Length 2088;  
Best Local Similarity 83.3%; Pred. No. 8.1e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCGTTC 6  
Db 1353 CCGTTC 1358

RESULT 8

US-09-548-367D-13  
Sequence 13, Application US/09548367D  
Patent No. 6440698  
GENERAL INFORMATION:  
APPLICANT: GURNEY ET AL.  
TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USE  
FILE REFERENCE: 29915/62801  
CURRENT APPLICATION NUMBER: US/09/548,367D  
CURRENT FILING DATE: 2000-04-12  
PRIOR APPLICATION NUMBER: US 60/155,493  
PRIOR FILING DATE: 1999-09-23  
PRIOR APPLICATION NUMBER: US 09/404,133  
PRIOR FILING DATE: 1999-09-23  
PRIOR APPLICATION NUMBER: PCT/US99/20881  
PRIOR FILING DATE: 1999-09-23  
PRIOR APPLICATION NUMBER: US 60/101,594  
PRIOR FILING DATE: 1998-09-24  
NUMBER OF SEQ ID NOS: 73  
SOFTWARE: Patentin version 3.1  
SEQ ID NO 13  
LENGTH: 2088  
TYPE: PRT

ORGANISM: Homo sapiens  
US-09-548-367D-13

Query Match  
Best Local Similarity 83.7%; Score 36; DB 4; Length 2088;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCGKTC 6  
11111  
DB 1353 CCGGTC 1358

RESULT 9  
US-09-201-227A-34  
Sequence 34, Application US/09201227A  
Patent No. 6468770  
GENERAL INFORMATION:  
APPLICANT: Keyes, Linda N.  
APPLICANT: Dobberstein, Stephen K.  
APPLICANT: Buchman, Andrew R.  
TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS OF D. MELANOGASTER INSULIN-LIKE,  
FILE REFERENCE: 7326-066  
CURRENT APPLICATION NUMBER: US/09/201,227A  
CURRENT FILING DATE: 1998-11-30  
NUMBER OF SEQ ID NOS: 45  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 34  
LENGTH: 24  
TYPE: PRT  
ORGANISM: Locust  
US-09-201-227A-34

Query Match  
Best Local Similarity 81.4%; Score 35; DB 4; Length 24;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCGKTC 6  
11111  
DB 9 CCRKTC 14

RESULT 10  
US-08-902-516-47  
Sequence 47, Application US/08902516  
Patent No. 5891432  
GENERAL INFORMATION:  
APPLICANT: SOO HOO, William  
TITLE OF INVENTION: MEMBRANE-BOUND CYTOKINE COMPOSITIONS  
TITLE OF INVENTION: COMPRISING GM-CSF AND METHODS OF MODULATING AN IMMUNE  
NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CAMPBELL & FLORES, LLP  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California  
COUNTRY: United States  
ZIP: 92121  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/902,516  
FILING DATE: 29-JUL-1997  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-1M 2442  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (619)535-9001  
TELEFAX: (619)535-8949  
INFORMATION FOR SEQ ID NO: 47:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 38 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-902-516-47

Query Match  
Best Local Similarity 81.4%; Score 35; DB 2; Length 38;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCGKTC 6  
11111  
DB 23 CCGGTC 28

RESULT 11  
US-09-201-227A-39  
Sequence 39, Application US/09201227A  
Patent No. 6468770  
GENERAL INFORMATION:  
APPLICANT: Keyes, Linda N.  
APPLICANT: Dobberstein, Stephen K.  
APPLICANT: Buchman, Andrew R.  
TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS OF D. MELANOGASTER INSULIN-LIKE  
FILE REFERENCE: 7326-066  
CURRENT APPLICATION NUMBER: US/09/201,227A  
CURRENT FILING DATE: 1998-11-30  
NUMBER OF SEQ ID NOS: 45  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 39  
LENGTH: 111  
TYPE: PRT  
ORGANISM: Locust  
FEATURE:  
NAME/KEY: SITE  
LOCATION: 34...85  
OTHER INFORMATION: Xaa = any amino acid  
US-09-201-227A-39

Query Match  
Best Local Similarity 81.4%; Score 35; DB 4; Length 111;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCGKTC 6  
11111  
DB 96 CCRKTC 101

RESULT 12  
US-09-738-884-1  
Sequence 1, Application US/09738884  
Patent No. 6391606  
GENERAL INFORMATION:  
APPLICANT: GUEGLER, Karl et al  
TITLE OF INVENTION: ISOLATED HUMAN PHOSPHOLIPASE PROTEINS,  
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PHOSPHOLIPASE  
FILE REFERENCE: C1000849  
CURRENT APPLICATION NUMBER: US/09/738,884  
CURRENT FILING DATE: 2000-12-18  
NUMBER OF SEQ ID NOS: 5  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1  
LENGTH: 2211  
TYPE: PRT  
ORGANISM: Human  
US-09-738-884-1

Query Match 81.4%; Score 35; DB 4; Length 2211;  
Best Local Similarity 83.3%; Pred. No. 1.1e+03;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCGKTC 6  
||| ||  
Db 63 CCGKTC 68

RESULT 13  
US-09-201-227A-37  
; Sequence 37, Application US/09201227A  
; Patent No. 6468770  
; GENERAL INFORMATION:  
; APPLICANT: Keyes, Linda N.  
; APPLICANT: Dobershtein, Stephen K.  
; APPLICANT: Buchman, Andrew R.  
; TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS OF D. MELANOGASTER INSULIN-LIKE  
; FILE REFERENCE: 7326-066  
; CURRENT APPLICATION NUMBER: US/09/201,227A  
; CURRENT FILING DATE: 1998-11-30  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 37  
; LENGTH: 124  
; TYPE: PRT  
; ORGANISM: Drosophila sp.  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: 43... 92  
; OTHER INFORMATION: Xaa - any amino acid  
US-09-201-227A-37

Query Match 79.1%; Score 34; DB 4; Length 124;  
Best Local Similarity 83.3%; Pred. No. 1.9e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCGKTC 6  
||| ||  
Db 107 CCGKTC 112

RESULT 14  
US-09-201-227A-4  
; Sequence 4, Application US/09201227A  
; Patent No. 6468770  
; GENERAL INFORMATION:  
; APPLICANT: Keyes, Linda N.  
; APPLICANT: Dobershtein, Stephen K.  
; APPLICANT: Buchman, Andrew R.  
; TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS OF D. MELANOGASTER INSULIN-LIKE  
; FILE REFERENCE: 7326-066  
; CURRENT APPLICATION NUMBER: US/09/201,227A  
; CURRENT FILING DATE: 1998-11-30  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 4  
; LENGTH: 154  
; TYPE: PRT  
; ORGANISM: Drosophila melanogaster  
US-09-201-227A-4

Query Match 79.1%; Score 34; DB 4; Length 154;  
Best Local Similarity 83.3%; Pred. No. 2.3e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCGKTC 6  
||| ||  
Db 137 CCGKTC 142

RESULT 15  
US-09-201-227A-18  
; Sequence 18, Application US/09201227A  
; Patent No. 6468770  
; GENERAL INFORMATION:  
; APPLICANT: Keyes, Linda N.  
; APPLICANT: Dobershtein, Stephen K.  
; APPLICANT: Buchman, Andrew R.  
; TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS OF D. MELANOGASTER INSULIN-LIKE  
; FILE REFERENCE: 7326-066  
; CURRENT APPLICATION NUMBER: US/09/201,227A  
; CURRENT FILING DATE: 1998-11-30  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 18  
; LENGTH: 154  
; TYPE: PRT  
; ORGANISM: Drosophila melanogaster  
US-09-201-227A-18

Query Match 79.1%; Score 34; DB 4; Length 154;  
Best Local Similarity 83.3%; Pred. No. 2.3e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCGKTC 6  
||| ||  
Db 137 CCGKTC 142

Search completed: May 6, 2003, 10:32:13  
Job time : 16 secs

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US-10-123-155-439
; Sequence 439, Application US/10123155
; Publication No. US20030068794A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Collin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C30
; CURRENT APPLICATION NUMBER: US/10/123,155
; CURRENT FILING DATE: 2002-04-15
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 439
; LENGTH: 434
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-123-155-439

Query Match      86.0%; Score 37; DB 9; Length 434;
Best Local Similarity 83.3%; Pred. No. 2.6e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CCGKTC 6
      ||| ||
      251 CCGATC 256

Db
```

```
US-10-123-155-401
; Sequence 401, Application US/10123155
; Publication No. US20030068794A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Collin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C30
; CURRENT APPLICATION NUMBER: US/10/123,155
; CURRENT FILING DATE: 2002-04-15
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 401

US-10-184-644-199
; Sequence 199, Application US/10184644
; Publication No. US20030044930A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Collin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C227
; CURRENT APPLICATION NUMBER: US/10/184,644
; CURRENT FILING DATE: 2002-06-28
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 199
; LENGTH: 636
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-184-644-199

Query Match      86.0%; Score 37; DB 9; Length 636;
Best Local Similarity 83.3%; Pred. No. 3.5e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CCGKTC 6
      ||| ||
      3 CCGTTC 8

Db
```



;; Prior Application removed - See File Wrapper or Palm  
;; NUMBER OF SEQ ID NOS: 612  
;; SEQ ID NO 199  
;; LENGTH: 636  
;; TYPE: DNA  
;; ORGANISM: Homo Sapien  
US-10-184-634-199

Query Match 86.0%; Score 37; DB 9; Length 636;  
Best Local Similarity 83.3%; Pred. No. 3.5e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CCGKTC 6  
||| ||  
Db 3 CCGTTC 8

RESULT 6  
US-10-184-644-255

;; Sequence 255, Application US/10184644  
;; Publication No. US20030044930A1  
;; GENERAL INFORMATION:

;; APPLICANT: Baker, Kevin P.  
;; APPLICANT: Chen, Jian  
;; APPLICANT: Desnoyers, Luc  
;; APPLICANT: Goddard, Audrey  
;; APPLICANT: Godowski, Paul J.  
;; APPLICANT: Gurney, Austin L.  
;; APPLICANT: Pan, James  
;; APPLICANT: Smith, Victoria  
;; APPLICANT: Watanabe, Colin K.  
;; APPLICANT: Wood, William I.  
;; APPLICANT: Zhang, Zemin  
;; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
;; FILE REFERENCE: P3430R1C227  
;; CURRENT APPLICATION NUMBER: US/10/184,644  
;; CURRENT FILING DATE: 2002-06-28  
;; Prior Application removed - See File Wrapper or Palm  
;; NUMBER OF SEQ ID NOS: 612  
;; SEQ ID NO 255  
;; LENGTH: 744  
;; TYPE: DNA  
;; ORGANISM: Homo Sapien  
US-10-184-644-255

Query Match 86.0%; Score 37; DB 9; Length 744;  
Best Local Similarity 83.3%; Pred. No. 3.9e+02;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CCGKTC 6  
||| ||  
Db 205 CCGTTC 210

RESULT 7  
US-10-184-634-255

;; Sequence 255, Application US/10184634  
;; Publication No. US20030068684A1  
;; GENERAL INFORMATION:

;; APPLICANT: Baker, Kevin P.  
;; APPLICANT: Chen, Jian  
;; APPLICANT: Desnoyers, Luc  
;; APPLICANT: Goddard, Audrey  
;; APPLICANT: Godowski, Paul J.  
;; APPLICANT: Gurney, Austin L.  
;; APPLICANT: Pan, James  
;; APPLICANT: Smith, Victoria  
;; APPLICANT: Watanabe, Colin K.  
;; APPLICANT: Wood, William I.  
;; APPLICANT: Zhang, Zemin  
;; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
;; TITLE OF INVENTION: ACIDS ENCODING THE SAME

;; FILE REFERENCE: P3430R1C217  
;; CURRENT APPLICATION NUMBER: US/10/184,634  
;; CURRENT FILING DATE: 2002-06-28  
;; Prior Application removed - See File Wrapper or Palm  
;; NUMBER OF SEQ ID NOS: 612  
;; SEQ ID NO 255  
;; LENGTH: 744  
;; TYPE: DNA  
;; ORGANISM: Homo Sapien  
US-10-184-634-255

Query Match 86.0%; Score 37; DB 9; Length 744;  
Best Local Similarity 83.3%; Pred. No. 3.9e+02;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CCGKTC 6  
||| ||  
Db 205 CCGTTC 210

RESULT 8  
US-10-184-644-125

;; Sequence 125, Application US/10184644  
;; Publication No. US20030044930A1  
;; GENERAL INFORMATION:

;; APPLICANT: Baker, Kevin P.  
;; APPLICANT: Chen, Jian  
;; APPLICANT: Desnoyers, Luc  
;; APPLICANT: Goddard, Audrey  
;; APPLICANT: Godowski, Paul J.  
;; APPLICANT: Gurney, Austin L.  
;; APPLICANT: Pan, James  
;; APPLICANT: Smith, Victoria  
;; APPLICANT: Watanabe, Colin K.  
;; APPLICANT: Wood, William I.  
;; APPLICANT: Zhang, Zemin  
;; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
;; FILE REFERENCE: P3430R1C227  
;; CURRENT APPLICATION NUMBER: US/10/184,644  
;; CURRENT FILING DATE: 2002-06-28  
;; Prior Application removed - See File Wrapper or Palm  
;; NUMBER OF SEQ ID NOS: 612  
;; SEQ ID NO 125  
;; LENGTH: 756  
;; TYPE: DNA  
;; ORGANISM: Homo Sapien  
US-10-184-644-125

Query Match 86.0%; Score 37; DB 9; Length 756;  
Best Local Similarity 83.3%; Pred. No. 4e+02;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CCGKTC 6  
||| ||  
Db 538 CCGTTC 543

RESULT 9  
US-10-184-634-125

;; Sequence 125, Application US/10184634  
;; Publication No. US20030068684A1  
;; GENERAL INFORMATION:

;; APPLICANT: Baker, Kevin P.  
;; APPLICANT: Chen, Jian  
;; APPLICANT: Desnoyers, Luc  
;; APPLICANT: Goddard, Audrey  
;; APPLICANT: Godowski, Paul J.  
;; APPLICANT: Gurney, Austin L.  
;; APPLICANT: Pan, James  
;; APPLICANT: Smith, Victoria  
;; APPLICANT: Watanabe, Colin K.  
;; APPLICANT: Wood, William I.

APPLICANT: Zhang,Zemin  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3430R1C217  
CURRENT APPLICATION NUMBER: US/10/184,634  
CURRENT FILING DATE: 2002-06-28  
Prior Application removed - See File Wrapper or Palm  
NUMBER OF SEQ ID NOS: 612  
SEQ ID NO: 125  
LENGTH: 756  
TYPE: DNA  
ORGANISM: Homo Sapien  
US-10-184-634-125

Query Match  
Best Local Similarity 86.0%; Score 37; DB 9; Length 756;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCGKTC 6  
DB 538 CCGATC 543

RESULT 10  
US-10-184-644-23  
Sequence 23, Application US/10184644  
Publication No. US20030044930A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Chen, Jian  
APPLICANT: Desnoyers, Luc  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Pan, James  
APPLICANT: Smith, Victoria  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3430R1C227  
CURRENT APPLICATION NUMBER: US/10/184,644  
CURRENT FILING DATE: 2002-06-28  
Prior Application removed - See File Wrapper or Palm  
NUMBER OF SEQ ID NOS: 612  
SEQ ID NO: 23  
LENGTH: 997  
TYPE: DNA  
ORGANISM: Homo Sapien  
US-10-184-644-23

Query Match  
Best Local Similarity 86.0%; Score 37; DB 9; Length 997;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCGKTC 6  
DB 10 CCGATC 15

RESULT 11  
US-10-184-634-23  
Sequence 23, Application US/10184634  
Publication No. US20030068684A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Chen, Jian  
APPLICANT: Desnoyers, Luc  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Pan, James

APPLICANT: Smith, Victoria  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3430R1C217  
CURRENT APPLICATION NUMBER: US/10/184,634  
CURRENT FILING DATE: 2002-06-28  
Prior Application removed - See File Wrapper or Palm  
NUMBER OF SEQ ID NOS: 612  
SEQ ID NO: 23  
LENGTH: 997  
TYPE: DNA  
ORGANISM: Homo Sapien  
US-10-184-634-23

Query Match  
Best Local Similarity 86.0%; Score 37; DB 9; Length 997;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCGKTC 6  
DB 10 CCGATC 15

RESULT 12  
US-10-123-155-315  
Sequence 315, Application US/10123155  
Publication No. US20030068794A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Beresini, Maureen  
APPLICANT: DeForge, Laura  
APPLICANT: Desnoyers, Luc  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Sherwood, Steven  
APPLICANT: Smith, Victoria  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Wood, William  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3330R1C30  
CURRENT APPLICATION NUMBER: US/10/123,155  
CURRENT FILING DATE: 2002-04-15  
Prior Application removed - See File Wrapper or Palm  
NUMBER OF SEQ ID NOS: 550  
SEQ ID NO: 315  
LENGTH: 1024  
TYPE: DNA  
ORGANISM: Homo Sapien  
US-10-123-155-315

Query Match  
Best Local Similarity 86.0%; Score 37; DB 9; Length 1024;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCGKTC 6  
DB 776 CCGATC 781

RESULT 13  
US-10-184-644-447  
Sequence 447, Application US/10184644

```
Publication No. US20030044930A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3430R1C227
CURRENT APPLICATION NUMBER: US/10/184,644
CURRENT FILING DATE: 2002-06-28
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 447
LENGTH: 1047
TYPE: DNA
ORGANISM: Homo Sapien
US-10-184-644-447
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Query Match
Best Local Similarity 86.0%; Score 37; DB 9; Length 1047;
Best Local Similarity 83.3%; Pred. No. 5.1e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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OY 1 CCGKTC 6
    ||| ||
Db 631 CCGTTC 636
```

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RESULT 14
US-10-184-634-447
Sequence 447, Application US/10184634
Publication No. US2003006864A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3430R1C217
CURRENT APPLICATION NUMBER: US/10/184,634
CURRENT FILING DATE: 2002-06-28
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 447
LENGTH: 1047
TYPE: DNA
ORGANISM: Homo Sapien
US-10-184-634-447
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```
Query Match
Best Local Similarity 86.0%; Score 37; DB 9; Length 1047;
Best Local Similarity 83.3%; Pred. No. 5.1e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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```
OY 1 CCGKTC 6
    ||| ||
Db 631 CCGTTC 636
```

```
RESULT 15
US-10-184-644-387
Sequence 387, Application US/10184644
Publication No. US20030044930A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3430R1C227
CURRENT APPLICATION NUMBER: US/10/184,644
CURRENT FILING DATE: 2002-06-28
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 387
LENGTH: 1094
TYPE: DNA
ORGANISM: Homo Sapien
US-10-184-644-387
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```
Query Match
Best Local Similarity 86.0%; Score 37; DB 9; Length 1094;
Best Local Similarity 83.3%; Pred. No. 5.3e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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OY 1 CCGKTC 6
    ||| ||
Db 343 CCGTTC 348
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Search completed: May 6, 2003, 10:36:39
Job time : 18 secs
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OM protein - protein search, using sw model

Run on: May 6, 2003, 10:27:25 ; Search time 44 Seconds  
(without alignments)  
13.109 Million cell updates/sec

Title: US-09-555-115A-66

Perfect score: 43

Sequence: 1 CCGKTC 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08  
Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR1:\*  
2: PIR2:\*  
3: PIR3:\*  
4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	93.0	214	2 T19930	hypothetical prote
2	37	86.0	151	2 E48552	US2 protein - infe
3	37	86.0	217	2 A88115	protein F53C3.5 [l
4	37	86.0	324	2 T24819	hypothetical prote
5	37	86.0	370	2 T37282	probable cathepsin
6	37	86.0	597	2 A32440	RNA-directed RNA P
7	37	86.0	1174	2 A39927	RNA-directed RNA P
8	37	86.0	4488	1 RRIH2	genome polyprotein
9	36	83.7	339	2 F8614	phenylalanine tRNA
10	36	83.7	339	2 B72011	phenylalanine tRNA
11	36	83.7	878	2 E85817	phenylalanine tRNA
12	35	81.4	37	2 S30985	gene 40 protein
13	35	81.4	276	2 T49220	casein kinase II (
14	35	81.4	283	2 T01595	casein kinase II (
15	35	81.4	333	2 AB3447	salicylaldehyde de
16	34	79.1	81	2 A45320	transglutaminase 8
17	34	79.1	96	2 JE0252	trypsin-6 - bovine
18	34	79.1	146	2 S53010	RCC2 protein - ric
19	34	79.1	151	2 S60314	RCC2 protein - ric
20	34	79.1	151	2 S60314	hair keratin cyste
21	34	79.1	159	2 T33696	hypothetical prote
22	34	79.1	186	2 A45910	ultra-high sulfur
23	34	79.1	186	2 T22278	hypothetical prote
24	34	79.1	190	2 T22279	hypothetical prote
25	34	79.1	192	1 TVGAC	transforming prote
26	34	79.1	192	2 A5492	GTP-binding protei
27	34	79.1	192	2 S54294	GTP-binding protei
28	34	79.1	192	2 G38625	GTP-binding protei
29	34	79.1	193	1 TVH012	GTP-binding protei

30	34	79.1	193	1 TVH012	GTP-binding protei
31	34	79.1	193	1 TVH012	GTP-binding protei
32	34	79.1	193	2 H36364	GTP-binding protei
33	34	79.1	196	1 TVH012	GTP-binding protei
34	34	79.1	196	1 TVH012	GTP-binding protei
35	34	79.1	196	1 TVH012	GTP-binding protei
36	34	79.1	202	2 JC5075	GTP-binding protei
37	34	79.1	205	2 JC4044	GTP-binding protei
38	34	79.1	205	2 T37769	rhodol-like protein
39	34	79.1	209	1 TVB011	transforming prote
40	34	79.1	265	2 T33695	hypothetical prote
41	34	79.1	340	2 T20148	probable cysteine
42	34	79.1	346	2 D47211	GTP-binding protei
43	34	79.1	347	2 T01044	hypothetical prote
44	34	79.1	400	2 B48613	surface protein SU
45	34	79.1	591	2 A99444	acylaminoacyl-pept
			611	2 A48582	vacuolar ATPase A

#### ALIGNMENTS

RESULT 1  
T19930  
hypothetical protein C44C10.9 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 18-Feb-2000  
C/Accession: T19930  
R:Coltage, A.  
submitted to the EMBL Data Library, February 1996  
A:Reference number: Z19197  
A/Accession: T19930  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-214 <RTL>  
A:Cross-references: EMBL:Z69787; PIDN:CAA93643.1; GSPDB:GN00028; CESP:C44C10.9  
A:Experimental source: clone C44C10  
C/Genetics:  
A:Gene: CESP:C44C10.9  
A:Map position: X  
A:Introns: 41/2; 64/2; 99/1; 152/2; 189/2

Query Match 93.0%; Score 40; DB 2; Length 214;  
Best Local Similarity 83.3%; Pred. No. 22;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGKTC 6  
DB 48 CCGKTC 53

RESULT 2  
E48552  
US2 protein - infectious laryngotracheitis virus  
C:Species: Infectious laryngotracheitis virus  
C>Date: 17-Feb-1994 #sequence\_revision 17-Feb-1994 #text\_change 29-Jan-1999  
C/Accession: E48552  
R:Sakaguchi, M.; Urahara, T.; Hirayama, Y.; Miki, N.; Yamamoto, M.; Hirai, K.  
Virus Genes 6: 365-378, 1992  
A:Title: Sequence determination and genetic content of an 8.9-kb restriction fragment  
A:Reference number: A48552; M01D:93118245; PMID:1282282  
A/Accession: E48552  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-151 <SAK>  
A>Note: sequence extracted from NCBI backbone (NCBI:121622, NCBI:121628)

Query Match 86.0%; Score 37; DB 2; Length 151;  
Best Local Similarity 83.3%; Pred. No. 50;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCGKTC 6  
DB 115 CCGKTC 120

RESULT 3  
A:Accession: A88115  
A:Protein F53C3.5 [Imported] - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 10-May-2001  
C:Accession: A88115  
R:Anonymous, The C. elegans Sequencing Consortium.  
S:Science 282, 2012-2018, 1998  
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biology  
A:Reference number: A75000; MUID:99069613; PMID:9851916  
A:Note: see websites genome.wustl.edu/gsc/C\_elegans/ and www.sanger.ac.uk/Projects/C\_elegans/  
A:Accession: A88115  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-217 <STO>  
A:Cross-references: GB:chr\_II; PIDN:AC67456.1; PID:93786483; GSPDB:GN00020; CESP:F53C3.5  
C:Genetics:  
A:Gene: F53C3.5  
A:Map position: 2

Query Match 86.0%; Score 37; DB 2; Length 217;  
Best Local Similarity 83.3%; Pred. No. 64;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CCGKTC 6  
DB 132 CCGKTC 137

RESULT 4  
T24819  
Hypothetical protein T10H4.12 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 21-Jan-2000  
C:Accession: T24819  
R:Baisham, V.  
S:submitted to the EMBL Data Library, October 1996  
A:Reference number: Z19938  
A:Accession: T24819  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-324 <WIL>  
A:Cross-references: EMBL:Z81119; PIDN:CAB03341.1; GSPDB:GN00023; CESP:T10H4.12  
A:Experimental source: clone T10H4  
C:Genetics:  
A:Gene: CESP:T10H4.12  
A:Map position: 5  
A:Introns: 184/1; 294/3  
C:Superfamily: papain

Query Match 86.0%; Score 37; DB 2; Length 324;  
Best Local Similarity 83.3%; Pred. No. 83;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CCGKTC 6  
DB 91 CCGKTC 96

RESULT 5  
T37282  
Probable cathepsin B (EC 3.4.22.1) cpr-3 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 21-Jul-2000  
C:Accession: T37282; T37283  
R:Larminie, C.G.; Johnstone, I.L.  
S:DNA Cell Biol. 15, 75-82, 1996  
A:Title: Isolation and characterization of four developmentally regulated cathepsin B-1  
A:Reference number: Z21662; MUID:96152242; PMID:8561899  
A:Accession: T37282

A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-370 <LAR>  
A:Cross-references: EMBL:L39925; PIDN:AAA98782.1  
A:Experimental source: strain Bristol NZ  
A:Accession: T37283  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-370 <LAR>  
A:Cross-references: EMBL:L39925; NID:9675493; PIDN:AAA98782.1; PID:9675494  
A:Experimental source: strain Bristol NZ  
C:Genetics:  
A:Gene: cpr-3  
A:Introns: 7/3; 230/1; 340/3  
C:Superfamily: papain  
C:Keywords: cysteine proteinase; hydrolase  
F:120,284,304/active site: Cys, His, Asn #status predicted

Query Match 86.0%; Score 37; DB 2; Length 370;  
Best Local Similarity 83.3%; Pred. No. 91;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CCGKTC 6  
DB 153 CCGKTC 158

RESULT 6  
A32440  
RNA-directed RNA polymerase (EC 2.7.7.48) - murine hepatitis virus (strain A59) (frag  
C:Species: murine hepatitis virus, MHV  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 18-Jun-1999  
C:Accession: A32440  
R:Pachuk, C.J.; Bredemeyer, P.J.; Zoltick, P.W.; Span, W.J.M.; Weiss, S.R.  
S:Virology 171, 141-148, 1989  
A:Title: Molecular cloning of the gene encoding the putative polymerase of mouse hepa  
A:Reference number: A32440; MUID:89299451; PMID:2545027  
A:Accession: A32440  
A:Molecule type: genomic RNA  
A:Residues: 1-597 <PAC>  
A:Cross-references: GB:M27198; NID:9928852; PIDN:AAA74011.1; PID:9928854  
C:Superfamily: coronavirus RNA-directed RNA polymerase  
C:Keywords: nucleotidyltransferase

Query Match 86.0%; Score 37; DB 2; Length 597;  
Best Local Similarity 83.3%; Pred. No. 1.2e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CCGKTC 6  
DB 390 CCGKTC 395

RESULT 7  
A39927  
RNA-directed RNA polymerase (EC 2.7.7.48) - murine hepatitis virus (strain MHV-A59 de  
C:Species: murine hepatitis virus, MHV  
C:Date: 29-Jan-1993 #sequence\_revision 29-Jan-1993 #text\_change 25-Oct-1996  
C:Accession: A39927  
R:van der Most, R.G.; Bredemeyer, P.J.; Spaan, W.J.M.  
S:J. Virol. 65, 3219-3226, 1991  
A:Title: A domain at the 3' end of the polymerase gene is essential for encapsidation  
A:Reference number: A39927; MUID:91237841; PMID:2033672  
A:Accession: A39927  
A:Molecule type: genomic RNA  
A:Residues: 1-1174 <VAN>  
A:Cross-references: GB:X57302  
A:Note: readthrough of the terminator UAA occurs between the codons GAU for residue 6  
C:Superfamily: coronavirus RNA-directed RNA polymerase  
C:Keywords: nucleotidyltransferase; RNA binding; RNA biosynthesis

Query Match 86.0%; Score 37; DB 2; Length 1174;  
Best Local Similarity 83.3%; Pred. No. 1.9e+02;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 CCGKTC 6  
11111  
Db 22 CCGDTC 27

RESULT 8  
RRIM2

genome polypeptide 1a - murine hepatitis virus (strain JHM)

N:Alternate names: 1a protein  
N:Contents: RNA-directed RNA polymerase (EC 2.7.7.48)

C:Species: murine hepatitis virus, MHV

C>Date: 30-Sep-1990 #sequence\_revision 31-Dec-1992 #text\_change 23-Mar-2001

C:Accession: A36815; A34072; A43572

R:Lee, H.J.; Shieh, C.K.; Gorbelenya, A.E.; Koonin, E.V.; La Monica, N.; Tuler, J.; Bagd  
submitted to Genbank, February 1991

A:Description: The complete sequence (22 kilobases) of murine coronavirus gene 1 encoding

A:Reference number: A36815

A:Accession: A36815

A:Molecule type: genomic RNA

A:Residues: 1-4488 <LEE>

A:Cross-references: GB:M55148; NID:g331851; PIDN:AAA46457.1; PID:g331852

R:Lee, H.J.; Shieh, C.K.; Gorbelenya, A.E.; Koonin, E.V.; La Monica, N.; Tuler, J.; Bagd

Virology 180, 567-582, 1991

A:Title: The complete sequence (22 kilobases) of murine coronavirus gene 1 encoding the

A:Reference number: A38547; MUID:91111976; PMID:1846489

A:Contents: annotation

A>Note: neither nucleotide nor complete amino acid sequence is given

R:See, L.H.; Shieh, C.K.; Baker, S.C.; Chang, M.F.; Lai, M.M.C.

J. Virol. 61, 3968-3976, 1987

A:Title: Sequence and translation of the murine coronavirus 5'-end genomic RNA reveals

A:Reference number: A34072; MUID:88062951; PMID:2824826

A:Accession: A34072

A:Molecule type: genomic RNA

A:Residues: 1-595 <SOE>

A:Cross-references: GB:M18040; NID:g331873; PIDN:AAA46466.1; PID:g555243

R:Baker, S.C.; La Monica, N.; Shieh, C.K.; Lai, M.M.C.

Adv. Exp. Med. Biol. 276, 283-289, 1990

A:Title: Murine coronavirus gene 1 polypeptide contains an autoproteolytic activity.

A:Reference number: A43572; MUID:91353364; PMID:1966414

A:Accession: A43572

A:Molecule type: genomic RNA

A:Residues: 1038-1343 <BAK>

A:Cross-references: GB:S51684; NID:g234107; PIDN:AA19566.1; PID:g234108

C:Genetics:

A:Gene: 1a

C:Superfamily: coronavirus RNA-directed RNA polymerase

C:Keywords: nucleic acid; transferase; RNA binding; RNA biosynthesis

Query Match

Best Local Similarity 86.0%; Score 37; DB 1; Length 4488;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCGKTC 6

11111

Db 390 CCGDTC 395

## RESULT 9

F86514 phenylalanyl tRNA synthetase, alpha [imported] - Chlamydia pneumoniae (strain J138)

C:Species: Chlamydia pneumoniae, Chlamydia pneumoniae

C>Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 23-Mar-2001

C:Accession: F86514

R:Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Is

Nucleic Acids Res. 28, 2311-2314, 2000

A:Title: Comparison of whole genome sequences of Chlamydia pneumoniae J138.

A:Reference number: A86491; MUID:20330349; PMID:10871362

A:Accession: F86514

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-339 <STO>

A:Cross-references: GB:BA000008; NID:g8979366; PIDN:BA99200.1; GSPDB:GN00142  
A:Experimental source: strain J138  
C:Genetics:  
A:Gene: pheS  
C:Superfamily: phenylalanyl-tRNA ligase alpha chain

Query Match 83.7%; Score 36; DB 2; Length 339;  
Best Local Similarity 83.3%; Pred. No. 1.2e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCGKTC 6  
11111  
Db 265 CCGKGC 270

## RESULT 10

B72011 phenylalanyl-tRNA ligase (EC 6.1.1.20) alpha chain [similarity] - Chlamydia pneumoniae

C:Species: Chlamydia pneumoniae, Chlamydia pneumoniae

C>Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 03-Jun-2002

C:Accession: B72011; F81529

R:Kaiman, S.; Mitchell, W.; Marathe, R.; Lamm, C.; Fan, J.; Olinger, L.; Grimwood,

Nature Genet. 21, 385-389, 1999

A:Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.

A:Reference number: A72000; MUID:99206606; PMID:10192388

A:Accession: B72011

A:Molecule type: DNA

A:Residues: 1-339 <ARN>

A:Cross-references: GB:AE001679; GB:AE001363; NID:g4377311; PIDN:AMD19130.1; PID:g437

A:Experimental source: strain CWL029

R:Read, T.D.; Brumham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hicke

C.; Dodson, R.; Gwinn, M.; Nelson, W.; Deboy, R.; Kolonay, J.; McClarty, G.; Salzbe

Nucleic Acids Res. 28, 1397-1406, 2000

A:Title: Genome sequences of Chlamydia trachomatis M09 and Chlamydia pneumoniae AR39

A:Reference number: A81500; MUID:20150255; PMID:10684355

A:Accession: F81529

A:Molecule type: DNA

A:Residues: 1-339 <REA>

A:Cross-references: GB:AE002245; GB:AE002161; NID:g7189769; PIDN:AAF36651.1; PID:g718

A:Experimental source: strain AR39, HL cells

C:Genetics:

A:Gene: pheS; CP0862

C:Superfamily: phenylalanyl-tRNA synthetase; ligase; protein biosynthesis

C:Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis

Query Match

Best Local Similarity 83.7%; Score 36; DB 2; Length 339;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCGKTC 6  
11111  
Db 265 CCGKGC 270

## RESULT 11

E85917 alanyl-tRNA synthetase [imported] - Escherichia coli (strain O157:H7, substrain EDL93

C:Species: Escherichia coli

C>Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 14-Sep-2001

C:Accession: E85917

R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May

hiller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda

Nature 409, 529-533, 2001

A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A:Reference number: A85480; MUID:21074935; PMID:11206551

A:Accession: E85917

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-878 <STO>

A:Cross-references: GB:AE005174; NID:g12517136; PIDN:AA657801.1; GSPDB:GN00145; UWGP:

A:Experimental source: strain O157:H7, substrain EDL933

C:Genetics:

A:Gene: alaS

C:Superfamily: alanine-tRNA ligase

Query Match 83.7%; Score 36; DB 2; Length 878;  
Best Local Similarity 83.3%; Pred. No. 2.3e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCGKTC 6  
|||||  
DB 857 CCGKTC 862

## RESULT 12

S30985  
gene 40 protein - Mycobacterium phage L5

C:Species: Mycobacterium phage L5

C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 08-Oct-1999

C:Accession: S30985

R:Donnelly-Wu, M.K.; Jacobs Jr, W.R.; Hatfull, G.F.

Mol. Microbiol. 7, 407-417, 1993

A:Title: Superinfection immunity of mycobacteriophage L5: applications for genetic trans

A:Reference number: S30949; MUID:93211283; PMID:8459767

A:Accession: S30985

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-37 <DON>

A:Cross-References: EMBL:Z18946; NID:g15859; PIDN:CAA79416.1; PID:g15896

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1992

C:Genetics:

A:Gene: 40

Query Match 81.4%; Score 35; DB 2; Length 37;  
Best Local Similarity 83.3%; Pred. No. 40;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCGKTC 6  
|||||  
DB 21 CCGKTC 26

## RESULT 13

T49220

casein kinase II (EC 2.7.1.-) beta chain CKB3 [validated] - Arabidopsis thaliana

N:Alternate names: protein F27H5.40

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Jun-2000 #sequence\_revision 02-Jun-2000 #text\_change 03-Nov-2000

C:Accession: T49220; T52032

R:Rieger, M.; Mueller-Auer, S.; Zipp, M.; Schaefer, M.; Mewes, H.W.; Rudd, S.; Lemcke, K

submitted to the Protein Sequence Database, April 2000

A:Reference number: Z25018

A:Accession: T49220

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-276 <RIE>

A:Cross-References: EMBL:AL163852; GSPDB:GN00061; ATSP:F27H5.40

A:Experimental source: cultivar Columbia; BAC clone F27H5

R: Sugano, S.; Andronis, C.; Green, R.M.; Wang, Z.Y.; Todin, E.M.

Proc. Natl. Acad. Sci. U.S.A. 95, 11020-5, 1998

A:Title: Protein kinase CK2 interacts with and phosphorylates the Arabidopsis circadian

A:Reference number: Z24495; MUID:9724832; PMID:9724832

A:Accession: T52032

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-276 <SUG>

A:Cross-References: EMBL:AF068318; PIDN:AAC33896.1

C:Genetics:

A:Gene: ATSP:F27H5.40

A:Map position: 3

A:Introns: 69/1; 142/1; 178/3; 234/1

A:Note: CKB3

A:Description: interacts specifically with circadian clock-associated 1 (CCA1) [validated]

A:Note: CKB3 is the only reported example of a third beta-subunit of CK2 found in any or

C:Keywords: phosphotransferase

Query Match 81.4%; Score 35; DB 2; Length 276;  
Best Local Similarity 66.7%; Pred. No. 1.5e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGKTC 6  
|||||  
DB 195 CCGKTC 200

## RESULT 14

T01595  
casein kinase II (EC 2.7.1.-) beta chain At2g44680 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 19-Feb-1999 #sequence\_revision 19-Feb-1999 #text\_change 16-Feb-2001

C:Accession: T01595; E84881

R:Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Syke

submitted to the EMBL Data Library, July 1998

A:Description: Arabidopsis thaliana chromosome II BAC F16B22 genomic sequence.

A:Reference number: Z14284

A:Accession: T01595

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-283 <ROU>

A:Cross-References: EMBL:AC003672; NID:g3341671; PID:g3341688

A:Experimental source: cultivar Columbia

R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanKen, S.E.; Umayam, L.; Tallon,

euss, D.; Nieman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter

Nature 402, 761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A:Reference number: A84420; MUID:20083487; PMID:10617197

A:Accession: E84881

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-283 <STO>

A:Cross-References: GB:AE002093; NID:g3341688; PIDN:AAC27470.1; GSPDB:GN00139

C:Genetics:

A:Map position: 2

A:Introns: 75/1; 148/1; 184/3; 240/1

C:Superfamily: human casein kinase II beta chain

C:Keywords: phosphotransferase; protein kinase

Query Match 81.4%; Score 35; DB 2; Length 283;  
Best Local Similarity 66.7%; Pred. No. 1.5e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGKTC 6  
|||||  
DB 201 CCGKTC 206

## RESULT 15

AB3447  
salicylaldehyde dehydrogenase (EC 1.-.-) [imported] - Brucella melitensis (strain 1

C:Species: Brucella melitensis

C:Date: 01-Feb-2002 #sequence\_revision 01-Feb-2002 #text\_change 01-Feb-2002

C:Accession: AB3447

R:DelVecchio, V.G.; Kapural, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanov

; Mazur, M.; Goldsman, E.; Selkov, E.; Elizer, P.H.; Hagius, S.; O'Callaghan, D.; Let

Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002

A:Title: The genome sequence of the facultative intracellular pathogen Brucella melit

A:Reference number: AB3447; PMID:11756688

A:Accession: AB3447

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-333 <KUR>

A:Cross-References: GB:AE008917; PIDN:AAL52741.1; PID:g17983572; GSPDB:GN00190

A:Experimental source: strain 16M

C:Genetics:

A:Gene: BME11560



A:Map position: I  
C:Keywords: oxidoreductase

Query Match 81.4%; Score 35; DB 2; Length 333;  
Best Local Similarity 66.7%; Pred. No. 1.7e+02;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 CCGKTC 6  
111: 1  
Db 12 CCGRAC 17

Search completed: May 6, 2003, 10:31:52  
Job time : 47 secs

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GenCore version 5.1.4-p5-4578  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 6, 2003, 10:17:40 ; Search time 11 Seconds

(without alignments)  
22.623 Million cell updates/sec

Title: US-09-555-115A-66

Perfect score: 43

Sequence: 1 CCGKTC 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwisProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	38	88.4	64	1	MTCU_CALSI
2	37	86.0	151	1	0453_HSVNG
3	37	86.0	370	1	CPRI_CABEL
4	37	86.0	597	1	RRPA_CWMA5
5	37	86.0	4488	1	RRPA_CWMAH
6	36	83.7	339	1	SYFA_CHLPN
7	35	81.4	37	1	VG40_BHML5
8	35	81.4	276	1	KC2D_ARATH
9	35	81.4	283	1	KC2E_ARATH
10	35	81.4	627	1	TESK_MOUSE
11	34	79.1	81	1	TRGS_TACTR
12	34	79.1	154	1	INL4_DROME
13	34	79.1	192	1	RHOI_DROME
14	34	79.1	192	1	RHOI_DROME
15	34	79.1	192	1	RHOI_DROME
16	34	79.1	192	1	RHOI_DROME
17	34	79.1	193	1	RHOI_DROME
18	34	79.1	193	1	RHOI_DROME
19	34	79.1	193	1	RHOI_DROME
20	34	79.1	193	1	RHOI_DROME
21	34	79.1	193	1	RHOI_DROME
22	34	79.1	193	1	RHOI_DROME
23	34	79.1	193	1	RHOI_DROME
24	34	79.1	193	1	RHOI_DROME
25	34	79.1	193	1	RHOI_DROME
26	34	79.1	193	1	RHOI_DROME
27	34	79.1	193	1	RHOI_DROME
28	34	79.1	193	1	RHOI_DROME
29	34	79.1	193	1	RHOI_DROME
30	34	79.1	193	1	RHOI_DROME
31	34	79.1	193	1	RHOI_DROME
32	34	79.1	193	1	RHOI_DROME
33	34	79.1	193	1	RHOI_DROME

34	34	79.1	1172	1	TRP2_MOUSE
35	34	79.1	3718	1	LMA5_MOUSE
36	33	76.7	37	1	TXOD_HADVE
37	33	76.7	60	1	MTA_CHAAC
38	33	76.7	76	1	VF07_VACCV
39	33	76.7	79	1	VF07_VACCV
40	33	76.7	80	1	VF07_VACCV
41	33	76.7	92	1	VF07_VACCV
42	33	76.7	102	1	ELAC_TRIVU
43	33	76.7	282	1	KC2C_ARATH
44	33	76.7	287	1	KC2E_ARATH
45	33	76.7	324	1	Y734_CHLPN

## ALIGNMENTS

RESULT 1  
MTCU\_CALSI STANDARD; PRT; 64 AA.  
AC 09U620;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Copper-specific metallothionein 2 (CuMT-II).  
OS Callinectes sapidus (Blue crab).  
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Crustacea;  
OC Malacostraca; Eumalacostraca; Eucarida; Decapoda; Pleocyemata;  
OC Brachyura; Eubrachyura; Portunoidae; Portunidae; Callinectes.  
OX NCBI\_Taxid-6763;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE-20356402; PubMed-10817938;  
RA Syring R.A., Hoexum-Brouwer T.H., Brouwer M.;  
RT Cloning and sequencing of cDNAs encoding for a novel copper-specific  
RT metallothionein and two cadmium-inducible metallothioneins from the  
RT blue crab Callinectes sapidus.  
RL Comp. Biochem. Physiol. 125C:325-332(2000).  
CC -1- FUNCTION: THE METALLOTHIONEINS ARE INVOLVED IN THE CELLULAR  
CC SEQUESTRATION OF TOXIC METAL IONS AND REGULATION OF ESSENTIAL  
CC TRACE ELEMENTS. THIS ISOFORM BINDS EXCLUSIVELY COPPER.  
CC -1- DOMAIN: 14 CYSTEINE RESIDUES ARE ARRANGED IN C-X-C GROUPS. THESE  
CC ARE THOUGHT TO BE THE METAL-BINDING SITES IN OTHER  
CC METALLOTHIONEINS.  
CC -1- SIMILARITY: BELONGS TO THE METALLOTHIONEIN SUPERFAMILY; FAMILY 2.  
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CC  
CC EMBL: AF200420; AF08966.1;  
CC InterPro: IPR001008; Mtlthion\_musc.  
CC InterPro: IPR001230; Ptenyl\_site.  
CC PRINTS: PR00875; MTMOUSC.  
CC Metal-binding: Metal-chelate cluster: Copper.  
CC SEQUENCE 64 AA: 6277 MW; B0B8767AD6CEB78A CR64;  
Query Match 88.4%; Score 38; DB 1; Length 64;  
Best local Similarity 83.3%; Pred. No. 7;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 CCGKTC 6  
DB 17 CCGSTC 22  
RESULT 2  
0453\_HSVNG STANDARD; PRT; 151 AA.  
ID 0453\_HSVNG

```

AC 005106:
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE Hypothetical 16.6 kDa protein.
GN US453
OS Marek's disease herpesvirus (strain GA) (MDHV).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Marek's disease-like viruses.
OX NCBI_TaxID=10388;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93118245; PubMed=1282282;
RA Sazaguchi M., Urakawa T., Hirayama Y., Miki N., Yamamoto M.,
RA Hirai K.;
RT "Sequence determination and genetic content of an 8.9-kb restriction
RT fragment in the short unique region and the internal inverted repeat
RT of Marek's disease virus type 1 DNA."
RL Virus Genes 6:365-378(1992).
CC -----
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CC -----
CC EMBL: M80595; AAB59894.1; -.
CC InterPro: IPR003485; US2_Unk.
CC Pfam: PF02476; US2; 1.
CC Hypothetical protein.
KM SEQUENCE 151 AA; 16635 MW; 5039D9E32D0D344C CRC64;
SQ
Query Match
Best Local Similarity 86.0%; Score 37; DB 1; Length 151;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 CCGKTC 6
DB 115 CCGKCC 120

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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: L39890; AAA98788.1; -.
CC EMBL: L39925; AAA98782.1; -.
CC EMBL: 281119; CAB61032.2; -.
CC EMBL: 282057; CAB61032.2; JOINED.
CC EMBL: 282057; CAB61024.2; -.
CC EMBL: 281119; CAB61024.2; JOINED.
CC HSP: P07688; 10DQ.
CC MEROPS: C01.0PA; -.
CC WormPep: T10H4.12; CE27590.
CC InterPro: IPR000668; Peptidase_C1.
CC InterPro: IPR000169; SHProt_acsite.
CC Pfam: PF00112; Peptidase_C1; 1.
CC PRINTS: PR00705; PAPA1N.
CC ProDom: PD000158; Peptidase_C1; 1.
CC PROSITE: PS00139; TH1OL_PROTEASE_CYS; 1.
CC PROSITE: PS00639; TH1OL_PROTEASE_HIS; 1.
CC PROSITE: PS00640; TH1OL_PROTEASE_ASN; 1.
CC KW Hydrolyase; Thiol protease; zymogen; signal.
FT SIGNAL 1
FT PROPEP 17
FT CHAIN 92
FT ACT_SITE 120
FT ACT_SITE 120
FT ACT_SITE 284
FT ACT_SITE 304
FT ACT_SITE 304
FT DISULFID 105
FT DISULFID 117
FT DISULFID 153
FT DISULFID 153
FT DISULFID 154
FT DISULFID 158
FT DISULFID 190
FT DISULFID 202
FT CARBOHYD 138
FT SEQUENCE 370 AA; 40770 MW; E6E50FE7C16F0867 CRC64;
SQ
Query Match
Best Local Similarity 86.0%; Score 37; DB 1; Length 370;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 CCGKTC 6
DB 153 CCGTTC 158

```

```

RESULT 3
CPR3_CAEEL STANDARD; PRT; 370 AA.
AC P43507; O9TW93;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Cathepsin B-like cysteine proteinase 3 precursor (EC 3.4.22.-)
DE (Cysteine protease related 3).
GN CPR-3 OR T10H4.12.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Bristol N2;
RA Larmann C.G.C., Johnstone I.L.;
RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-Bristol N2;
RA Baahm V.M.;
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP REVISIONS.
RA Dublin R.;
CC Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C1.
CC -----

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RESULT 4
RPPA_CVMA5 STANDARD; PRT; 597 AA.
ID RPPA_CVMA5
AC P19750;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE RNA-directed RNA polymerase (ORF1) (EC 2.7.7.48) (Fragment).
OS Murine coronavirus MHV (strain A59).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
OX NCBI_TaxID=11142;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89299451; PubMed=2545027;
RA Pachuk C.J., Bredenbeek P.J., Zoltick P.W., Spaan W.J.M., Weiss S.R.;
RT "Molecular cloning of the gene encoding the putative polymerase of
RT mouse hepatitis coronavirus, strain A59."
RL Virology 171:141-148(1989).
CC -1- FUNCTION: THE RNA DEPENDENT RNA POLYMERASE OF CORONAVIRUSES IS
CC A MULTIFUNCTIONAL PROTEIN. IT CONTAINS THE ACTIVITIES NECESSARY
CC FOR THE TRANSCRIPTION OF NEGATIVE STRANDED RNA, LEADER RNA,
CC SUBGENOMIC MRNAs AND PROGENY VIRION RNA.
CC -----

```

CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate - N diphosphate +  
CC (RNA)(N).  
CC -----  
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CC -----  
DR EMBL: M27198; AAA74011.1; -  
DR PIR: A32440; A32440.  
KW Transferase; RNA-directed RNA polymerase.  
FT NON\_TER 597 597  
SQ SEQUENCE 597 AA; 66193 MW; 165D4FACAA3BC49E CRC64;  
  
Query Match 86.0%; Score 37; DB 1; Length 597;  
Best Local Similarity 83.3%; Pred. No. 48;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 CCGKTC 6  
DB 390 CCGDTC 395  
ID SYFA\_CVMJH STANDARD; PRT; 4488 AA.  
AC P19751; 066194; (Rel. 17, Created)  
DT 01-FEB-1991 (Rel. 25, Last sequence update)  
DT 01-APR-1993 (Rel. 38, Last annotation update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE RNA-directed RNA polymerase (ORF1A) (EC 2.7.7.48).  
OS Murine coronavirus MHV (strain JHM).  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;  
OC Coronaviridae; Coronavirus.  
OX NCBI\_TaxID=11144;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE-9111976; PubMed-1846489;  
RA Lee H.-J., Shieh C.-K., Gorbalenya A.E., Koonin E.V., Ia Monica N.,  
RA Tuler J., Bagdzhadzhyan A., Lai M.-M.C.;  
RT "The complete sequence (22 kilobases) of murine coronavirus gene 1  
RT encoding the putative proteases and RNA polymerase.";  
RL Virology 180:567-582(1991).  
RN [2]  
RP SEQUENCE OF 1-595 FROM N.A.  
RX MEDLINE-88062951; PubMed-2824826;  
RA Soe L.H., Shieh C.K., Baker S.C., Chang M.F., Lai M.-M.C.;  
RT "Sequence and translation of the murine coronavirus 5'-end genomic  
RT RNA reveals the N-terminal structure of the putative RNA  
RT polymerase.";  
RL J. Virol. 61:3968-3976(1987).  
RN [3]  
RP FUNCTION: THE RNA DEPENDENT RNA POLYMERASE OF CORONAVIRUSES IS  
CC A MULTIFUNCTIONAL PROTEIN: IT CONTAINS THE ACTIVITIES NECESSARY  
CC FOR THE TRANSCRIPTION OF NEGATIVE STRANDED RNA, LEADER RNA,  
CC SUBGENOMIC MRNAS AND PROGENY VIRION RNA.  
CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate - N diphosphate +  
CC (RNA)(N).  
CC -----  
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CC -----  
DR EMBL: M55148; AAA6457.1; -  
DR EMBL: M18040; AAA6466.1; -  
DR PIR: A36815; RRIHM2.  
DR MEROPS: C16.001; -

DR MEROPS: C29.001; -  
DR MEROPS: C30.001; -  
DR InterPro: IPR002589; Alpp.  
DR InterPro: IPR002705; Peptidase\_C16.  
DR Pfam: PF01661; Alpp; 1.  
DR Pfam: PF01831; Peptidase\_C16; 1.  
DR SMART: SM00506; Alpp; 1.  
KW Transferase; RNA-directed RNA polymerase.  
SQ SEQUENCE 4488 AA; 499890 MW; D9EE61A9E2141799 CRC64;  
  
Query Match 86.0%; Score 37; DB 1; Length 4488;  
Best Local Similarity 83.3%; Pred. No. 2e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 CCGKTC 6  
DB 390 CCGDTC 395  
ID SYFA\_CHLPPN STANDARD; PRT; 339 AA.  
AC Q926R6;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Phenylalanyl-tRNA synthetase alpha chain (EC 6.1.1.20) (Phenylalanine-  
DE tRNA ligase alpha chain) (PheRS).  
GN PHE-OR CPN0993 OR CP0862.  
OS Chlamydia pneumoniae (Chlamydia pneumoniae).  
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.  
OX NCBI\_TaxID=83558;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX SPRAIN-CW1029.  
RC MEDLINE-99206606; PubMed-10192388;  
RA Kaiman S., Mitchell W., Marathe R., Lammell C., Fan J., Hyman R.W.,  
RA Olinger L., Grimwood J., Davis R.W., Stephens R.S.;  
RT "Comparative genomes of Chlamydia pneumoniae and C. trachomatis.";  
RL Nat. Genet. 21:385-389(1999).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN-AR39.  
RX MEDLINE-20150255; PubMed-10684935;  
RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,  
RA White O., Hickey E.K., Peterson J., Ufferback T., Berry K., Bass S.,  
RA Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,  
RA Eisen J., Fraser C.M.;  
RT "Genome sequences of Chlamydia trachomatis MOpn and Chlamydia  
RT pneumoniae AR39.";  
RL Nucleic Acids Res. 28:1397-1406(2000).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN-Q138.  
RX MEDLINE-2030349; PubMed-10871362;  
RA Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,  
RA Shiba T., Ishi K., Hattori M., Kuhara S., Nakazawa T.;  
RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138  
RT from Japan and CW1029 from USA.";  
RL Nucleic Acids Res. 28:2311-2314(2000).  
RN [4]  
RP -1- CATALYTIC ACTIVITY: ATP + L-phenylalanine + tRNA(Phe) - AMP +  
CC diphosphate + L-phenylalanyl-tRNA(Phe).  
CC -1- SUBUNIT: Tetramer of two alpha and two beta chains (BY  
CC SIMILARITY).  
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
CC -1- SIMILARITY: BELONGS TO CLASS-II AMINOACYL-TRNA SYNTHETASE FAMILY.  
CC PHE-TRNA SYNTHETASE ALPHA CHAIN SUBFAMILY 1.  
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 CC -----  
 DR EMBL: AE001679; AAD19130.1; -  
 DR EMBL: AE002245; AAF38651.1; -  
 DR EMBL: AP002548; BAA99200.1; -  
 DR HSSP: P27001; 1B7Y.  
 DR TIGR: CP0862; -  
 DR InterPro: IPR002106; ALCRNA\_LigaseII.  
 DR InterPro: IPR004529; Phes.  
 DR InterPro: IPR004188; Phe\_tRNA\_synth\_N.  
 DR InterPro: IPR002319; tRNA-synth\_2d.  
 DR Pfam: PF01409; tRNA-synth\_2d; 1.  
 DR Pfam: PF02912; Phe\_tRNA-synth\_N; 1.  
 DR TIGRfams: TIGR00468; Phes; 1.  
 DR PROSITE: PS00862; AA.TRNA.LIGASE.II; 1.  
 KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;  
 KW Complete proteome.  
 SQ SEQUENCE 339 AA; 38366 MW; D7BA5917EAD9C2A CRC64;

Query Match 83.7%; Score 36; DB 1; Length 339;  
 Best Local Similarity 83.3%; Pred. No. 46;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCGKTC 6  
 DB 265 CCGKTC 270

RESULT 7  
 VC40\_BPML5 STANDARD; PRT; 37 AA.  
 ID VG40\_BPML5  
 AC 005250;  
 DT 01-FEB-1994 (Rel. 28, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 01-FEB-1994 (Rel. 28, Last annotation update)  
 DE Gene 40 protein (GP40).  
 GN 40.  
 OS Mycobacteriophage L5.  
 OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;  
 OC L5-like viruses.  
 OC NCBI\_TaxID=31757;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93211282; PubMed=8459766;  
 RA Hatfull G.F., Sarkis G.J.;  
 RT "DNA sequence, structure and gene expression of mycobacteriophage L5:  
 RT a phage system for mycobacterial genetics.";  
 RL Mol. Microbiol. 7:395-405(1993).  
 CC -----

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 CC -----  
 DR EMBL: 218946; CAA79416.1; -  
 DR PIR: S30985; S30985.  
 SQ SEQUENCE 37 AA; 4444 MW; 0A3696C8418AFCE CRC64;

Query Match 81.4%; Score 35; DB 1; Length 37;  
 Best Local Similarity 83.3%; Pred. No. 13;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCGKTC 6  
 DB 21 CCGKTC 26

RESULT 8

KC2D\_ARATH STANDARD; PRT; 276 AA.  
 ID KC2D\_ARATH  
 AC 081275;  
 DT 15-JUL-1999 (Rel. 38, Created)  
 DT 15-JUL-1999 (Rel. 38, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Casein kinase II beta-3 chain (CK II).  
 GN CKB3 OR A13G60250 OR F27H5\_40.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 CC euroids II; Brassicales; Brassicaceae; Arabidopsids.  
 OC NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98393763; PubMed=9724822;  
 RX Sugeno S., Andronis C., Green R.M., Wang Z.Y., Tobin E.M.;  
 RT "Protein Kinase CK2 interacts with and phosphorylates the Arabidopsids  
 RT circadian clock-associated 1 protein.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 95:11020-11025(1998).  
 [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cy. Columbia;  
 RX MEDLINE=21016720; PubMed=11130713;  
 RA Salanoubat M., Lemcke K., Rieger M., Ansoerge W., Unselid M.,  
 RA Faltmann B., Valle G., Bloecker H., Perez-Alonso M., Obermayer B.,  
 RA Delseny M., Boutry M., Grievell L.A., Mache R., Puldomenech P.,  
 RA De Simone V., Cholsne N., Artiguenave F., Robert C., Brottier P.,  
 RA Winkler P., Cattolico L., Welschbach J., Saurin W., Quetier F.,  
 RA Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,  
 RA Wurdach E., Drzonek H., Erle H., Jordan N., Bangert S.,  
 RA Wiedelmann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,  
 RA Vezzi A., D'Angelo M., Pallavicini A., Toppo S., Simionati B.,  
 RA Conrad A., Hornischer K., Kauer G., Loehner T.-H., Nordstiek G.,  
 RA Reichelt J., Scharfe M., Schoen O., Barges M., Terol J., Clement J.,  
 RA Navarro P., Collado C., Perez-Perez A., Ottenweider B., Duchemin D.,  
 RA Cooke R., Lande M., Berger-Liauro C., Purnelle B., Masny D.,  
 RA de Haan M., Maarse A.C., Alcaraz J.-P., Cottet A., Casacuberta E.,  
 RA Monfort A., Argirou A., Flores M., Liguori R., Vitale D.,  
 RA Manhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Mewes H.-W.,  
 RA Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,  
 RA Rooney T., Rizzo M., Walts A., Uterback T., Fujii C.Y., Shea T.P.,  
 RA Creasy T.H., Haas B., Maiti R., Wu D., Peterson J., Van Aken S.,  
 RA Pal G., Miltischer J., Sellers P., Gall J.E., Feldblyum T.V.,  
 RA Preuss D., Lin X., Niernan W.C., Salzberg S.L., White O., Venter J.C.,  
 RA Fraser C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asamizu E.,  
 RA Sasamoto S., Kimura T., Idesawa K., Kawashima K., Kishida Y.,  
 RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Muraki A.,  
 RA Watanabe S., Nakazaki N., Shimpo S., Takeuchi C., Wada T.,  
 RA Watanabe A., Yamada M., Yasuda M., Tabata S.;  
 RT "Sequence and analysis of chromosome 3 of the plant Arabidopsis  
 RT thaliana.";  
 RL Nature 406:820-822(2000).  
 CC -1- FUNCTION: PLAYS A COMPLEX ROLE IN REGULATING THE BASAL CATALYTIC  
 CC ACTIVITY OF THE ALPHA SUBUNIT (BY SIMILARITY).  
 CC -1- SUBUNIT: TETRAMER COMPOSED OF AN ALPHA CHAIN, AN ALPHA', AND  
 CC TWO BETA-TYPE CHAINS.  
 CC -1- SIMILARITY: BELONGS TO THE CASEIN KINASE 2 BETA CHAIN FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL: AF068318; AAC3896.1; -  
 DR EMBL: AL163852; CAB87862.1; -  
 DR TRANSFAC: T02899; -  
 DR InterPro: IPR000704; CAS\_kinase\_II.  
 DR Pfam: PF01214; CK\_II\_beta; 1.

DR PRINTS: PR00472; CASNKINASEII.  
 DR PROSITE: PS01101; CK2\_BETA.1.  
 KW Transferase; Serine/threonine-protein kinase; Phosphorylation.  
 SQ SEQUENCE 276 AA; 30798 MW; 611FPC1222B2CC55 CRC64;

Query Match 81.4%; Score 35; DB 1; Length 276;  
 Best Local Similarity 66.7%; Pred. NO. 56;  
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCGKTC 6  
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 Db 195 CCGGSC 200

RESULT 9  
 KC2E\_ARATH STANDARD; PRT; 283 AA.  
 ID KC2E\_ARATH  
 AC 080507;  
 DT 15-JUL-1999 (Rel. 38, Created)  
 DT 15-JUL-1999 (Rel. 38, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Putative casein kinase II beta-4 chain (CK II).  
 GN AT2G44680 OR F16B2.17.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicot; Rosidae;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 NC NCB1\_Taxid=3702;  
 RX MEDLINE=20083487; PubMed=10617197;  
 RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,  
 RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblum T.V.,  
 RA Beil C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L.,  
 RA Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam L.,  
 RA Taiton L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,  
 RA Goodman M.C., Somerville C.R., Copenhaver G.P., Preuss D.,  
 RA Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,  
 RA Venter J.C.;  
 RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis  
 thaliana.";  
 RT Nature 402:761-768(1999).  
 RL Nature 402:761-768(1999).  
 CC -1- FUNCTION: PLAYS A COMPLEX ROLE IN REGULATING THE BASAL CATALYTIC  
 CC ACTIVITY OF THE ALPHA SUBUNIT (BY SIMILARITY).  
 CC -1- SUBUNIT: TETRAMER COMPOSED OF AN ALPHA CHAIN, AN ALPHA', AND  
 CC TWO BETA-TYPE CHAINS.  
 CC -1- PFM: PHOSPHORYLATED BY ALPHA CHAIN (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE CASEIN KINASE 2 BETA CHAIN FAMILY.  
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 CC -----  
 CC EMBL: AC003672; AAC27470.1; -;  
 CC InterPro: IPR000704; CAS\_kinase\_II.  
 CC Pfam: PF01214; CK\_II\_beta.1.  
 CC PRINTS: PR00472; CASNKINASEII.  
 DR PROSITE: PS01101; CK2\_BETA.1.  
 KW Transferase; Serine/threonine-protein kinase; Phosphorylation.  
 SQ SEQUENCE 283 AA; 31631 MW; DF5811A78F060797 CRC64;

Query Match 81.4%; Score 35; DB 1; Length 283;  
 Best Local Similarity 66.7%; Pred. NO. 57;  
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCGKTC 6  
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 Db 201 CCGGSC 206

RESULT 10  
 TASK\_MOUSE STANDARD; PRT; 627 AA.  
 ID TASK\_MOUSE  
 AC 070146; 070147;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Testis-specific protein kinase 1 (EC 2.7.1.1).  
 GN TEST1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NC NCB1\_Taxid=10090;  
 RX MEDLINE=98137797; PubMed=9469938;  
 RA Toshima J., Nakagawara K.-I., Mori M., Noda T., Mizuno K.;  
 RT "Structural organization and chromosomal localization of the mouse  
 RT test1 (testis-specific protein kinase 1) gene.";  
 RL Gene 206:237-245(1998).  
 CC -1- FUNCTION: DISPLAYS SERINE/THREONINE-SPECIFIC PHOSPHORYLATION OF  
 CC MYELIN BASIC PROTEIN (MBP) AND HISTONE IN VITRO. PROBABLY PLAYS A  
 CC CENTRAL ROLE AT AND AFTER THE MEIOTIC PHASE OF SPERMATOGENESIS  
 CC (BY SIMILARITY).  
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: 1 (SHOWN HERE) AND 2; ARE  
 CC PRODUCED BY ALTERNATIVE SPLICING.  
 CC -1- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN TESTIS.  
 CC -1- DOMAIN: THE CATALYTIC C-TERMINAL PART IS HIGHLY RICH IN  
 CC PROLINE RESIDUES.  
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
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 CC -----  
 CC EMBL: AB003493; BAA25124.1; -;  
 CC EMBL: AB003494; BAA25125.1; -;  
 CC MGD: MGI:1201675; Test1.  
 CC InterPro: IPR000719; Euk\_Pkinase.  
 CC InterPro: IPR001245; Tyr\_Pkinase.  
 CC Pfam: PF00069; Pkinase.1.  
 CC ProDom: PD000001; Euk\_Pkinase.1.  
 DR PROSITE: PS01017; PROTEIN\_KINASE\_ATP.1.  
 DR PROSITE: PS0011; PROTEIN\_KINASE\_DOM.1.  
 DR PROSITE: PS00109; PROTEIN\_KINASE\_TYR.1.  
 KW Transferase; Serine/threonine-protein kinase; ATP-binding;  
 KW Alternative splicing.  
 FT DOMAIN 52 309  
 FT NP\_BIND 58 66  
 FT BINDING 81 81  
 FT ACT\_SITE 170 170  
 FT VARSPIC 203 260  
 FT KGORSPFWLWAPRTGMLORCCGSCMMRRMSSPGSSSV  
 FT SSSPEYLTITTVLVR -> EGRKEPLAVGSPYMWAPR  
 FT VLRGELYDERKADVFAGFIVLCETLIRVPADPDYLRPE  
 FT (IN ISOFORM 2).  
 SQ SEQUENCE 627 AA; 68094 MW; A582B39629485AAB CRC64;

Query Match 81.4%; Score 35; DB 1; Length 627;  
 Best Local Similarity 66.7%; Pred. NO. 99;  
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCGKTC 6  
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 Db 223 CCGGSC 228

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RESULT 11
TRGS_TACTR STANDARD; PRT; 81 AA.
AC P81281;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DE 8.6 kDa Transglutaminase substrate.
OS Tachypleus tridentatus (Japanese horseshoe crab).
OC Tachypleus: Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;
OC Limulidae; Tachypleus.
OX NCBI_TaxID=6853;
RN [1]
RP SEQUENCE.
RC TISSUE=Hemocyte;
RX MEDLINE=93107011; PubMed=8093242;
RA Tokunaga F., Yamada M., Miyata T., Ding Y.L., Hirnaga-Kavabata M.,
RA Muta T., Iwanaga S., Ichinose A., Davie E.W.;
RT "Limulus hemocyte transglutaminase. Its purification and
RT characterization, and identification of the intracellular
RT substrates."
RL J. Biol. Chem. 268:252-261(1993).
CC -1- SUBUNIT: MULTIMERIC.
DR InterPro: IPR000867; Insl_gro_fac-pr.
DR SMART: SM00121; IB; 1.
KW Hemolymph.
SQ SEQUENCE 81 AA; 8672 MW; 4E2BE4794A7D01B1 CRC64;

Query Match 79.1%; Score 34; DB 1; Length 81;
Best Local Similarity 83.3%; Pred. No. 33;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CCGKTC 6
DB 39 CAGKTC 44

RESULT 12
INLA_DROME STANDARD; PRT; 154 AA.
AC Q9VT50;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Probable insulin-like peptide 4 precursor.
GN CG14173.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Cealinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Chame M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abbill J.F., Adysani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
RA Baller R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,
RA Burlis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Fabios B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Doudson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Gary N.S., Gelbart W.M., Glasser K.,
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,

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RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laske P., Lei Y., Levitsky A.C., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Mikhina N.V., Modyarty C., Morris J., Mostreli A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclet J.M.,
RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svitskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao O.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Zhu H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
CC -1- SUBCELLULAR LOCATION: Secreted (Potential).
CC -1- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
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CC -----
DR EMBL: AE003550; AAF50205.1; -.
DR HSSP: P01343; IGFI.
DR Flybase: FBgn0036045; CG14173.
DR InterPro: IPR004825; Ins/IGF/relax.
DR Pfam: PF00049; Insulin; 1.
DR SMART: SM00078; IIGF; 1.
DR PROSITE: PS00262; INSULIN; 1.
KW Insulin family; Cleavage on pair of basic residues; Signal.
FT FT SIGNAL 1 29 POTENTIAL.
FT FT CHAIN 30 154 PROBABLE INSULIN-LIKE PEPTIDE 4.
FT FT CHAIN 30 69 PROBABLE INSULIN-LIKE PEPTIDE 4 B CHAIN
FT FT CHAIN 125 154 (POTENTIAL).
FT FT PROPEP 73 122 CONNECTING PEPTIDE (POTENTIAL).
FT FT DISULFID 49 138 PROBABLE INSULIN-LIKE PEPTIDE 4 A CHAIN
FT FT DISULFID 61 151 INTERCHAIN (BY SIMILARITY).
FT FT DISULFID 137 142 INTERCHAIN (BY SIMILARITY).
SQ SEQUENCE 154 AA; 16851 MW; 65E78F17EDC12041 CRC64;

Query Match 79.1%; Score 34; DB 1; Length 154;
Best Local Similarity 83.3%; Pred. No. 52;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CCGKTC 6
DB 137 CCGKTC 142

RESULT 13
RH01_DROME STANDARD; PRT; 192 AA.
AC P48148; Q9V3J0;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ras-like GTP-binding protein RH01.
GN RH01 OR CG8416.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

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NCBI\_TaxID-7227;  
 [1]  
 SEQUENCE FROM N.A.  
 MEDLINE-95137009; PubMed-7835340;  
 Harlaren I.K., Hu K.-Q., Asha H., Quintanilla A., Ezzell R.M.,  
 Settlemann J.,  
 "Characterization of rho GTPase family homologues in Drosophila  
 melanogaster: overexpressing Rho1 in retinal cells causes a late  
 developmental defect.";  
 RT  
 EMBL J. 14:292-302(1995).  
 [2]  
 SEQUENCE FROM N.A.  
 MEDLINE-20025334; PubMed-10556060;  
 Magie C.R., Meyer M.R., Gorsuch M.S., Parkhurst S.M.,  
 "Mutations in the Rho1 small GTPase disrupt morphogenesis and  
 segmentation during early Drosophila development.";  
 RT  
 Development 126:5353-5364(1999).  
 [3]  
 SEQUENCE FROM N.A.  
 STRAIN-Berkeley;  
 RC  
 MEDLINE-20196006; PubMed-10731132;  
 Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 Sutton G.G., Wortman J.R., Fandell M.D., Zhang Q., Chen L.X.,  
 Brandon R.C., Rogers J.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,  
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 Hostin D., Houston K.A., Howland T.J., Wei M.-H., Iqbal C.,  
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 Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 "The genome sequence of Drosophila melanogaster.";  
 RT  
 Science 287:2185-2195(2000).  
 [1]  
 SIMILARITY: BELONGS TO THE SMALL GTPASE SUPERFAMILY. RHO FAMILY.  
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 EMBL: L38311; AAA67042.1; -  
 EMBL: AF177871; AAF01183.1; -  
 DR EMBL: AF177872; AAF01184.1; -  
 DR EMBL: AF177873; AAF01185.1; -

EMBL: AF177874; AAF01186.1; -  
 DR EMBL: AEO03808; AAF58066.1; -  
 DR HSSP: P06749; 1FTN.  
 DR FlyBase: FBgn0014020; Rho1.  
 DR InterPro: IPR003578; GTPase\_Rho.  
 DR InterPro: IPR001230; Prenyl\_site.  
 DR InterPro: IPR001806; Ras\_tnsfing.  
 DR InterPro: IPR005225; Small\_GTP.  
 DR Pfam: PF00071; ras; 1.  
 DR Pfam: PR00449; RASTRNSFRMG.  
 DR SMART: SM00174; RHO; 1.  
 DR TIGRfam: TIGR00231; small\_GTP; 1.  
 KW GTP-binding; Prenylation; Lipoprotein.  
 FT NP\_BIND 12 19 GTP (BY SIMILARITY).  
 FT NP\_BIND 59 63 GTP (BY SIMILARITY).  
 FT NP\_BIND 117 120 GTP (BY SIMILARITY).  
 FT DOMAIN 34 42 EFFECTOR REGION (POTENTIAL).  
 FT LIPID 189 189 GERANYL-GERANYL (BY SIMILARITY).  
 FT SEQUENCE 192 AA; 21723 MW; B89C7D884E1743CF CRC64;  
 SQ  
 Query Match 79.1%; Score 34; DB 1; Length 192;  
 Best Local Similarity 100.0%; Pred. No. 61;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 CGKTC 6  
 DB 16 CGKTC 20  
 ID RHOA\_CAEEL STANDARD; PRT; 192 AA.  
 AC Q22038;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE RAS-like GTP-binding protein RhoA.  
 GN RHO-1 OR RHOA OR Y51H4A.3.  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;  
 OC Rhabditidae; Meloiderinae; Caenorhabditis.  
 OC NCBI\_TaxID-6239;  
 RX MEDLINE-95096090; PubMed-7798239;  
 RA Chen W., Lim L.;  
 RT "The Caenorhabditis elegans small GTP-binding protein RhoA is  
 RT enriched in the nerve ring and sensory neurons during larval  
 RT development.";  
 RT J. Biol. Chem. 269:32394-32404(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-Bristol N2;  
 RA Submitted J.E.;  
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
 CC -1- SUBCELLULAR LOCATION: ASSOCIATED WITH THE MEMBRANE AND THE  
 CC CYTOSKELETON THROUGHOUT DEVELOPMENT.  
 CC -1- DEVELOPMENTAL STAGE: UBIQUITOUS EXPRESSION THROUGHOUT DEVELOPMENT  
 CC WITH A PARTICULAR ENRICHMENT AT LARVAL STAGES IN THE PHARYNGEAL  
 CC NERVE RING AND AT THE TIP OF THE HEAD CONTAINING CHEMOSENSORY AND  
 CC MECHANOSENSORY NEURONS.  
 CC -1- SIMILARITY: BELONGS TO THE SMALL GTPASE SUPERFAMILY. RHO FAMILY.  
 -----  
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 -----  
 EMBL: L36965; AAC37216.1; -

DR EMBL: AL132952; CAB63379.1; -.  
 DR HSSP: P06749; IFTN.  
 DR Wormpep: Y51H4A.3; CE25369.  
 DR InterPro: IPR003578; GTPase\_Rho.  
 DR InterPro: IPR001230; Prenyl\_site.  
 DR InterPro: IPR001806; Ras\_trnsfrmng.  
 DR InterPro: IPR005225; Small\_GTP.  
 DR Pfam: PF00071; ras; 1.  
 DR SMART: PR00449; RASTRNSFRMNG.  
 DR SMART: SM00174; RHO; 1.  
 DR TIGRFAMs: TIGR00231; small\_GTP; 1.  
 DR GTP-binding; Prenylation; Lipoprotein.  
 FT NP\_BIND 12 19 GTP (BY SIMILARITY).  
 FT NP\_BIND 59 63 GTP (BY SIMILARITY).  
 FT NP\_BIND 117 120 GTP (BY SIMILARITY).  
 FT DOMAIN 34 42 GTP (BY SIMILARITY).  
 FT LIPID 189 189 EFFECTOR REGION (POTENTIAL).  
 FT LIPID 189 189 GERANYL-GERANYL (BY SIMILARITY).  
 SQ SEQUENCE 192 AA; 21635 MW; 0B10A744BD0CF81 CRC64;

Query Match 79.1%; Score 34; DB 1; Length 192;  
 Best Local Similarity 100.0%; Pred. No. 61;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 CGKTC 6  
 |||||  
 DB 16 CGKTC 20

RESULT 15  
 RHO\_APLICA  
 ID RHO\_APLICA STANDARD; PRT: 192 AA.  
 AC P01122;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 01-OCT-1994 (Rel. 30, Last annotation update)  
 DE RAS-like GTP-binding protein RHO.  
 GN RHO.  
 OS Aplysia californica (California sea hare).  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Opisthobranchia; Anaspiidae;  
 OC Aplysidae; Aplysia.  
 OX NCBI\_TaxID=6500;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=85201682; PubMed=3888408;  
 RA Madanle P., Axel R.;  
 RT "A novel ras-related gene family.";  
 RL Cell 41:31-40(1985).  
 CC -! SIMILARITY: BELONGS TO THE SMALL GTPASE SUPERFAMILY. RHO FAMILY.  
 CC -----  
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 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC -----  
 CC EMBL: M10078; AAA27776.1; -.  
 DR PIR: A01373; TVGAC.  
 DR HSSP: P06749; IFTN.  
 DR InterPro: IPR003578; GTPase\_Rho.  
 DR InterPro: IPR001230; Prenyl\_site.  
 DR InterPro: IPR001806; Ras\_trnsfrmng.  
 DR Pfam: PF00071; ras; 1.  
 DR PRINTS: PR00449; RASTRNSFRMNG.  
 DR SMART: SM00174; RHO; 1.  
 DR TIGRFAMs: TIGR00231; small\_GTP; 1.  
 DR GTP-binding; Prenylation; Lipoprotein.  
 FT NP\_BIND 12 19 GTP (BY SIMILARITY).  
 FT NP\_BIND 59 63 GTP (BY SIMILARITY).  
 FT NP\_BIND 117 120 GTP (BY SIMILARITY).  
 FT DOMAIN 34 42 GTP (BY SIMILARITY).  
 FT LIPID 189 189 EFFECTOR REGION (POTENTIAL).  
 FT LIPID 189 189 GERANYL-GERANYL (BY SIMILARITY).  
 SQ SEQUENCE 192 AA; 21661 MW; 669024366AA3AA21 CRC64;

FT LIPID 189 189 GERANYL-GERANYL (BY SIMILARITY).  
 SQ SEQUENCE 192 AA; 21661 MW; 669024366AA3AA21 CRC64;

Query Match 79.1%; Score 34; DB 1; Length 192;  
 Best Local Similarity 100.0%; Pred. No. 61;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 CGKTC 6  
 |||||  
 DB 16 CGKTC 20

Search completed: May 6, 2003, 10:29:29  
 Job time: 13 secs



AC 08T0H3:  
 DT 01-JUN-2002 (TREMBLrel. 21, Created)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE LD03740P.  
 GN P120CTN.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 NX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BERKELEY;  
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,  
 RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,  
 RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,  
 RA Nunoo J., Pacle J., Paragas V., Park S., Phouanavong S., Wan K.,  
 RA Yu C., Lewis S.E., Rubin G.M., Celinker S.,  
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY0659321; AAL39466.1;  
 SQ SEQUENCE 562 AA; 62937 MW; 4FEC238370923C CRC64;

Query Match 90.7%; Score 39; DB 5; Length 562;  
 Best Local Similarity 83.3%; Pred. No. 16;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCGKTC 6  
 DB 153 CCGETC 158

## RESULT 3

O9W5T9 PRELIMINARY; PRT; 779 AA.

AC O9W5T9:  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
 DE Putative P120CTN protein (CG17484 protein).  
 GN P120CTN OR CG17484.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 NX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BERKELEY;  
 RA MEDLINE-20196006; PubMed-10731132;  
 RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amenatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA Abail J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
 RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotler P.,  
 RA Burlis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Dudin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,  
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwan C.,  
 RA Jajall M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Lasako P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,

RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Klimos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of Drosophila melanogaster."  
 RL Science 287:2185-2195(2000).  
 DR EMBL; AE002751; AAF45461.1;  
 DR HSSP; P35222; 1G3T  
 DR P120CTN OR CG17484.  
 DR Flybase; FBgn0015587; p120ctn.  
 DR InterPro; IPR000225; Armadillo.  
 DR Pfam; PF00514; Armadillo\_seg; 4.  
 DR SMART; SM00185; ARM; 3.  
 DR PROSITE; PSS0176; ARM\_REPEAT; 3.  
 KW Hypothetical protein.  
 SQ SEQUENCE 779 AA; 86588 MW; 5A1F546AE055CC2B CRC64;

Query Match 90.7%; Score 39; DB 5; Length 779;  
 Best Local Similarity 83.3%; Pred. No. 21;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCGKTC 6  
 DB 340 CCGETC 345

## RESULT 4

O9NHPI PRELIMINARY; PRT; 781 AA.

AC O9NHPI:  
 DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
 DE Putative P120CTN protein (CG17484 protein).  
 GN P120CTN OR CG17484.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 NX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC Cavallo R., Myster S., Pelfer M.;  
 RT "A Drosophila melanogaster homolog of the adherens junction protein p120ctn."  
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF220496; AAF33245.1;  
 DR HSSP; P35222; 1G3T.  
 DR Flybase; FBgn0015587; p120ctn.  
 DR InterPro; IPR000225; Armadillo.  
 DR Pfam; PF00514; Armadillo\_seg; 5.  
 DR SMART; SM00185; ARM; 3.  
 DR PROSITE; PSS0176; ARM\_REPEAT; 3.  
 SQ SEQUENCE 781 AA; 86836 MW; 5F8888EA349C7CEE CRC64;

Query Match 90.7%; Score 39; DB 5; Length 781;  
 Best Local Similarity 83.3%; Pred. No. 21;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCGKTC 6  
 DB 372 CCGETC 377

## RESULT 5

ID	Q9GNM6	PRELIMINARY:	PRT:	196 AA.
AC	Q9GNM6:			
DT	01-MAR-2001 (TREMBLrel. 16, Created)			
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)			
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)			
DE	Purative cathepsin B.5 (Fragment).			
GN	CATB.5.			
OS	Ostertagia ostertagi.			
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;			
OC	Trichostrongyloidea; Haemonchidae; Ostertagiinae; Ostertagia.			
OX	NCBI_TaxID=6317;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Geldhof P.B., Vercauteren I.J.R., Peelaers I., Agneessens J.,			
RA	Claeerebout E., Vercruyssen J.;			
RT	"Molecular and biochemical characterization of cathepsin B enzymes in			
RT	Ostertagia ostertagi.";			
RL	Submitted (OCT-2000) to the EMBL/Genbank/DBJ databases.			
DR	EMBL: AJ296148; CAC13131.1; -.			
DR	HSSP: P07688; 10DQ.			
DR	InterPro: IPR000668; Peptidase_C1.			
DR	InterPro: IPR001230; Prenyl_site.			
DR	InterPro: IPR000169; SHprot_acsite.			
DR	Pfam: PF00112; Peptidase_C1; 1.			
DR	ProDom: PD000158; Peptidase_C1; 1.			
DR	PROSITE: PS00294; PRENYLATION; UNKNOWN_1.			
DR	PROSITE: PS00639; THIOL_PROTEASE_HIS; 1.			
FT	NON_TER	1		
FT	NON_TER	1		
SO	SEQUENCE	196 AA; 21114 MW; F2B57E2865EB2DF2 CRC64;		
QY	1 CCGKTC 6	86.0%; Score 37; DB 5; Length 196;		
DB	35 CCGKRC 40	Best Local Similarity 83.3%; Pred. NO. 15;		
		Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		
QY	1 CCGKTC 6	86.0%; Score 37; DB 4; Length 205;		
DB	11111 1	Best Local Similarity 83.3%; Pred. NO. 16;		
		Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		
QY	1 CCGKTC 6	86.0%; Score 37; DB 4; Length 205;		
DB	11111 1	Best Local Similarity 83.3%; Pred. NO. 16;		
		Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		

DB	50	CCGKRC	55	
RESULT 7				
ID	029897	PRELIMINARY;	PRT;	211 AA.
AC	029897			
DT	01-JAN-1998 (TREMBLrel. 05, Created)			
DT	01-JAN-1998 (TREMBLrel. 05, Last sequence update)			
DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)			
DE	Conserved hypothetical transmembrane protein.			
GN	AF0350.			
OS	Archaeoglobus fulgidus.			
OC	Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;			
OC	Archaeoglobaceae; Archaeoglobus.			
OX	NCBI_TaxID=2234;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-VC-16 / DSM 4304 / ATCC 49558;			
RX	MEDLINE-96049343; PubMed-9389475;			
RA	Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,			
RA	Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.R., Peterson J.D.,			
RA	Richardson D.L., Kervlavage A.R., Graham D.E., Kyriides N.C.,			
RA	Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,			
RA	Kirness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,			
RA	Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodok A., Zhou L.,			
RA	Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Uitterback T.,			
RA	Saiton P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,			
RA	Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,			
RA	Venter J.C.;			
RT	"The complete genome sequence of the hyperthermophilic, sulphate-			
RT	reducing archaeon Archaeoglobus fulgidus.";			
RL	Nature 390:364-370(1997).			
DR	EMBL: AE001080: AAB90884.1; -			
DR	TIGR: AF0350; -			
DR	InterPro: IPR002781; DUF81.			
DR	Pfam: PF01925; DUF81; 1.			
KW	Hypothetical protein; Transmembrane; Complete proteome.			
SQL	SEQUENCE 211 AA; 23303 MW; 927825BC1EFC1B46 CRC64;			
Query Match 86.0%; Score 37; DB 17; Length 211;				
Best Local Similarity 83.3%; Pred. No. 16;				
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;				
QY	1	CGGTC 6		
DB	80	CCGKRC 85		
RESULT 8				
Q9TXT4		PRELIMINARY;	PRT;	217 AA.
ID	Q9TXT4			
AC	Q9TXT4			
DT	01-MAY-2000 (TREMBLrel. 13, Created)			
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)			
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE	Hypothetical 24.4 kDa protein.			
GN	F53C3.5.			
OS	Caenorhabditis elegans.			
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;			
OC	Rhabditidae; Pelodidae; Caenorhabditis.			
OX	NCBI_TaxID=6239;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-BRISTOL N2;			
RX	MEDLINE-99069613; PubMed-9851916;			
RA	None;			
RT	"Genome sequence of the nematode C. elegans: a platform for			
RT	investigating biology. The C. elegans Sequencing Consortium.";			
RL	Science 282:2012-2018(1998).			
RN	[2]			
RP	SEQUENCE FROM N.A.			

RC STRAIN-BRISTOL NZ;  
 RA Murray J., Wohlmann P., Bauer C., Antoniou B.;  
 RT "The sequence of C. elegans cosmid F53C3.";  
 RL Submitted (OCT-1998) to the EMBL/Genbank/DBJ databases.  
 RN [13]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BRISTOL NZ;  
 RA Waterston R.;  
 RT "Direct Submission.";  
 RL Submitted (SEP-2001) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: AF098992; AAC67456.1; -  
 DR InterPro: IPR002619; CX.  
 DR Pfam: PF01705; CX; 1.  
 DR ProDom: PD006744; CX; 1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 217 AA; 24433 MW; 03BF85067036933C CRC64;

Query Match 86.0%; Score 37; DB 5; Length 217;  
 Best Local Similarity 83.3%; Pred. NO. 17;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCGKTC 6  
 DB 132 CCGKTC 137

RESULT 9  
 Q69285 PRELIMINARY; PRT; 270 AA.  
 AC Q69285;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE US2 protein.  
 GN US2.  
 OS Turkey herpesvirus.  
 CC Viruses: dsDNA viruses, no RNA stage; Herpesviridae;  
 CC Alphaherpesvirinae; Marek's disease-like viruses.  
 OX NCBI\_TaxID=10390;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=9513166; PubMed=7831788;  
 RA Brnovskis P., Velicer L.F.;  
 RT "The Marek's disease virus (MDV) unique short region: alpha herpesvirus-homologous, fowlpox virus-homologous, and MDV-specific genes.";  
 RL Virology 206:324-338(1995).  
 DR EMBL: L22174; AAA64964.1; -  
 DR InterPro: IPR000169; SHprot\_acsite.  
 DR InterPro: IPR003485; US2\_unk.  
 DR Pfam: PF02476; US2; 1.  
 DR PROSITE: PS00639; THIOI\_PROTEASE\_HIS; UNKNOWN.1.  
 SQ SEQUENCE 270 AA; 29735 MW; 47F36676ED75B74 CRC64;

Query Match 86.0%; Score 37; DB 12; Length 270;  
 Best Local Similarity 83.3%; Pred. NO. 20;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCGKTC 6  
 DB 234 CCGKTC 239

RESULT 10  
 Q9E6L9 PRELIMINARY; PRT; 270 AA.  
 AC Q9E6L9;  
 DT 01-MAR-2001 (TREMBLrel. 16, Created)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE HSV1 US2.  
 GN MDV091.  
 OS Turkey herpesvirus.

OC Viruses: dsDNA viruses, no RNA stage; Herpesviridae;  
 OC Alphaherpesvirinae; Marek's disease-like viruses.  
 OX NCBI\_TaxID=10390;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-MDS;  
 RA MEDLINE=20392152; PubMed=10933706;  
 RA Tulman E.R., Afonso C.L., Lu Z., Zsak L., Rock D.L., Kutish G.F.;  
 RT "The genome of a very virulent Marek's disease virus.";  
 RL J. Virol. 74:7980-7988(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-MDS;  
 RA Tulman E.R., Afonso C.L., Lu Z., Zsak L., Rock D.L., Kutish G.F.;  
 RL Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: AF243438; AAG14265.1; -  
 DR InterPro: IPR000169; SHprot\_acsite.  
 DR InterPro: IPR003485; US2\_unk.  
 DR Pfam: PF02476; US2; 1.  
 DR PROSITE: PS00639; THIOI\_PROTEASE\_HIS; UNKNOWN.1.  
 SQ SEQUENCE 270 AA; 29848 MW; A5556D8E872E731F CRC64;

Query Match 86.0%; Score 37; DB 12; Length 270;  
 Best Local Similarity 83.3%; Pred. NO. 20;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCGKTC 6  
 DB 234 CCGKTC 239

RESULT 11  
 Q8SZU1 PRELIMINARY; PRT; 407 AA.  
 AC Q8SZU1;  
 DT 01-JUN-2002 (TREMBLrel. 21, Created)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE GH10778P.  
 OS Drosophila melanogaster (Fruit fly).  
 CC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 CC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 CC Ephydriidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BERKELEY;  
 RA Stapleton M., Brokstein P., Hong L., Aghayani A., Carlson J.,  
 RA Champagne M., Chavez C., Dorsett V., Dresner D., Farfan D., Frise E.,  
 RA George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,  
 RA Miranda A., Mungall C.J., Nunoo J., Paclebo J., Paragas V., Park S.,  
 RA Patel S., Phoumanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,  
 RA Ceiliker S.;  
 RL Submitted (DEC-2001) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: AY070508; AAL47979.1; -  
 SQ SEQUENCE 407 AA; 46046 MW; 4CF766081CEDC60F CRC64;

Query Match 86.0%; Score 37; DB 5; Length 407;  
 Best Local Similarity 83.3%; Pred. NO. 28;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCGKTC 6  
 DB 349 CCGKTC 354

RESULT 12  
 Q9J3E9 PRELIMINARY; PRT; 4467 AA.  
 AC Q9J3E9;  
 DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)

DE RNA-directed RNA polymerase.  
OS murine hepatitis virus.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;  
OC Coronaviridae; Coronavirus.  
OX NCBI\_TaxID-11138;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-MV-10;  
RA Das Sarma J., Hingley S.T., Lai M.M.C., Weiss S.R., Lavi E.;  
RT "Pathogenesis and sequence analysis of mouse hepatitis virus type 2;  
RT an experimental model system of acute meningitis and hepatitis in  
RT mice."  
RT Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF208067; AAF69341.1; -  
DR MEROPS: C29.001; -  
DR MEROPS: C30.001; -  
DR InterPro: IPR002589; Alpp.  
DR InterPro: IPR002705; Peptidase\_C16.  
DR InterPro: IPR000504; RNA\_rec\_mot.  
DR Pfam: PF01661; Alpp; 1.  
DR Pfam: PF01831; Peptidase\_C16; 1.  
DR SMART: SM00506; Alpp; 1.  
DR PROSITE: PS00030; RRM\_RNP\_1; UNKNOWN\_1.  
KM RNA-directed RNA polymerase.  
SQ SEQUENCE 4467 AA; 496337 MW; 0F4CD64E7E2D7146 CRC64;

Query Match 86.0%; Score 37; DB 12; Length 4467;  
Best Local Similarity 83.3%; Pred. No. 2.1e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CCGKTC 6  
DB 387 CCGDTC 392

RESULT 13  
ID 039225 PRELIMINARY; PRT; 4470 AA.  
AC 039225;  
DT 01-JAN-1998 (TREMBLrel. 05, Created)  
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE RNA-directed RNA polymerase.  
OS murine hepatitis virus.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;  
OC Coronaviridae; Coronavirus.  
OX NCBI\_TaxID-11138;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-MHV-A59;  
RC MEDLINE-98087821; PubMed-9426441;  
RA Leparc-Goffart I., Hingley S.T., Chua M.M., Jiang X., Lavi E.,  
RA Weiss S.R.;  
RT "Altered pathogenesis of a mutant of the murine coronavirus MHV-A59 is  
RT associated with a Q159L amino acid substitution in the spike  
RT protein."  
RT Virology 239:1-10(1997).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN-MHV-A59;  
RA Weiss S.R., Leparc-Goffart I., Hingley S.T.;  
RT Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF029248; AAB86820.1; -  
DR InterPro: IPR002589; Alpp.  
DR InterPro: IPR002705; Peptidase\_C16.  
DR Pfam: PF01661; Alpp; 1.  
DR Pfam: PF01831; Peptidase\_C16; 1.  
DR SMART: SM00506; Alpp; 1.  
KM RNA-directed RNA polymerase.  
SQ SEQUENCE 4470 AA; 496513 MW; 8DE2E9BDF663FAF CRC64;

Query Match 86.0%; Score 37; DB 12; Length 4470;  
Best Local Similarity 83.3%; Pred. No. 2.1e+02;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 1 CCGKTC 6  
DB 390 CCGDTC 395

RESULT 14  
ID 09BPA0 PRELIMINARY; PRT; 83 AA.  
AC 09BPA0;  
DT 01-JUN-2001 (TREMBLrel. 17, Created)  
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE Conotoxin scaffold VI/VII.  
OS Conus ventricosus (Mediterranean cone).  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;  
OC Neogastropoda; Conoidea; Conidae; Conus.  
OX NCBI\_TaxID-117992;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC MEDLINE-21105969; PubMed-1158371;  
RA Conticello S.G., Gild Y., Avidan N., Ben-Asher E., Levy Z.,  
RA Faltzliber M.;  
RT "Mechanisms for Evolving Hypervariability: The Case of Conopeptides."  
RT Mol. Biol. Evol. 18:120-131(2001).  
DR EMBL: AF215037; AAG60465.1; -  
DR InterPro: IPR004214; Conotoxin.  
DR Pfam: PF02950; Conotoxin; 1.  
SQ SEQUENCE 83 AA; 9403 MW; D53923EACE4E1974 CRC64;

Query Match 83.7%; Score 36; DB 5; Length 83;  
Best Local Similarity 83.3%; Pred. No. 11;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CCGKTC 6  
DB 73 CCGGTC 78

RESULT 15  
ID 061515 PRELIMINARY; PRT; 348 AA.  
AC 061515;  
DT 01-AUG-1998 (TREMBLrel. 07, Created)  
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)  
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)  
DE Cathepsin B-like cysteine protease GCF7.  
GN GCF7.  
OS Haemonchus contortus (Barber pole worm).  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;  
OC Trichostrongyloidea; Haemonchidae; Haemonchinae; Haemonchus.  
OX NCBI\_TaxID-6289;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-OSDA BELTSVILLE; TISSUE-INTESTINE;  
RA Rehman A., Jaaser D.P.;  
RT Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF046229; AAC05262.1; -  
DR HSP: P07688; IODO.  
DR MEROPS: C01.101; -  
DR InterPro: IPR000668; Peptidase\_C1.  
DR InterPro: IPR000169; SHprot\_acste.  
DR Pfam: PF00112; Peptidase\_C1; 1.  
DR PRINTS: PR00705; PAPAIN.  
DR PRODOM: PD000158; Peptidase\_C1; 1.  
DR PROSITE: PS00139; THIOL\_PROTEASE\_CYS; UNKNOWN\_1.  
DR PROSITE: PS00639; THIOL\_PROTEASE\_HIS; UNKNOWN\_1.  
KM Protease.  
SQ SEQUENCE 348 AA; 39176 MW; 6AFD85F084B5DF5 CRC64;

Query Match 83.7%; Score 36; DB 5; Length 348;  
Best Local Similarity 83.3%; Pred. No. 36;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 CCGKTC 6  
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Db 157 CCGKFC 162

Search completed: May 6, 2003, 10:31:02  
Job time : 88 secs





GenCore version 5.1.4\_p5\_4578  
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OM protein - protein search, using sw model

Run on: May 6, 2003, 10:29:16 ; Search time 143 Seconds  
(without alignments)  
27.052 Million cell updates/sec

Title: US-09-555-115A-66

Perfect score: 43  
Sequence: 1 CCGKTC 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 4569144 segs, 644733110 residues

Total number of hits satisfying chosen parameters: 4569144

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

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27: /cgn2\_6/ptodata/1/paa/US06\_COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	43	100.0	6	US-09-555-115A-66	Sequence 66, App1
2	43	100.0	103	US-09-270-767-34140	Sequence 34140, A
3	43	100.0	103	US-09-270-767-49357	Sequence 49357, A
4	43	100.0	103	US-09-270-849B-180217	Sequence 180217, A
5	39	90.7	121	US-09-688-052-3216	Sequence 3216, App
6	39	90.7	475	US-09-270-767-46709	Sequence 46709, A

7	39	90.7	561	16	US-09-270-767-42679	Sequence 42679, A
8	39	90.7	672	16	US-09-270-767-46165	Sequence 46165, A
9	39	90.7	779	20	US-09-614-150-25746	Sequence 25746, A
10	39	90.7	779	21	US-09-791-537-81601	Sequence 81601, A
11	39	90.7	779	27	US-60-191-637-25876	Sequence 25876, A
12	39	90.7	779	27	US-60-191-681-20485	Sequence 20485, A
13	39	90.7	781	21	US-09-791-537-104827	Sequence 104827, A
14	38	88.4	232	16	PCT-US99-08504-28	Sequence 28, App1
15	38	86.0	27	17	US-09-298-102-28	Sequence 131, App
16	37	86.0	27	17	PCT-US01-23041A-131	Sequence 354, App
17	37	86.0	27	23	PCT-US01-23041A-131	Sequence 131, App
18	37	86.0	27	23	US-09-910-082A-131	Sequence 354, App
19	37	86.0	27	23	US-09-910-082A-131	Sequence 354, App
20	37	86.0	31	24	US-10-072-602B-154	Sequence 154, App
21	37	86.0	31	24	US-10-072-602B-154	Sequence 154, App
22	37	86.0	39	20	US-09-611-197-139	Sequence 139, App
23	37	86.0	72	1	PCT-US01-23041A-130	Sequence 130, App
24	37	86.0	72	23	US-09-910-082A-130	Sequence 130, App
25	37	86.0	76	24	US-10-072-602B-153	Sequence 153, App
26	37	86.0	102	1	PCT-US01-29871-159	Sequence 159, App
27	37	86.0	102	1	PCT-US02-08123-1416	Sequence 1416, App
28	37	86.0	102	1	PCT-US02-08123-1792	Sequence 1792, App
29	37	86.0	102	1	PCT-US02-08124-585	Sequence 585, App
30	37	86.0	102	1	PCT-US02-08124-740	Sequence 740, App
31	37	86.0	102	1	PCT-US02-08276-439	Sequence 439, App
32	37	86.0	102	1	PCT-US02-08276-561	Sequence 561, App
33	37	86.0	102	1	PCT-US02-08277-920	Sequence 920, App
34	37	86.0	102	1	PCT-US02-08277-1170	Sequence 1170, App
35	37	86.0	102	1	PCT-US02-08278-1357	Sequence 1357, App
36	37	86.0	102	1	PCT-US02-08278-1719	Sequence 1719, App
37	37	86.0	102	1	PCT-US02-09785-995	Sequence 995, App
38	37	86.0	102	1	PCT-US02-09785-781	Sequence 781, App
39	37	86.0	102	25	US-10-103-295-159	Sequence 159, App
40	37	86.0	103	1	PCT-US01-00911-158	Sequence 158, App
41	37	86.0	103	1	PCT-US99-15849-158	Sequence 158, App
42	37	86.0	103	18	US-09-482-273-158	Sequence 158, App
43	37	86.0	103	23	US-09-984-271-158	Sequence 158, App
44	37	86.0	103	23	US-09-984-276-158	Sequence 158, App
45	37	86.0	151	21	US-09-791-537-80760	Sequence 80760, A

#### ALIGNMENTS

RESULT 1  
US-09-555-115A-66  
Sequence 66, Application US/09555115A  
GENERAL INFORMATION:  
APPLICANT: Bonach, Gregory I.  
TITLE OF INVENTION: NON-TOXIC IMMUNE STIMULATING ENTEROTOXIN COMPOSITIONS  
FILE REFERENCE: 12136, US06  
CURRENT APPLICATION NUMBER: US/09/555, 115A  
CURRENT FILING DATE: 2000-08-01  
PRIOR APPLICATION NUMBER: PCT/US98/25107  
PRIOR FILING DATE: 1998-12-01  
PRIOR APPLICATION NUMBER: US 60/067,357  
PRIOR FILING DATE: 1997-12-02  
NUMBER OF SEQ ID NOS: 66  
SOFTWARE: Patent version 3.1  
SEQ ID NO 66  
LENGTH: 6  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic  
US-09-555-115A-66

Query Match 100.0%; Score 43; DB 19; Length 6;  
Best Local Similarity 100.0%; Pred. No. 4,2e+06;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
1 CCGKTC 6  
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Db 1 CCGKTC 6

RESULT 2  
US-09-270-767-34140

Sequence 34140, Application US/09270767

GENERAL INFORMATION:

APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*

FILE REFERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 34140

LENGTH: 103

TYPE: PRT

ORGANISM: *Drosophila melanogaster*

US-09-270-767-34140

Query Match

Best Local Similarity 100.0%; Score 43; DB 16; Length 103;  
Pred. No. 1.9e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCGKTC 6

Db 87 CCGKTC 92

RESULT 3

US-09-270-767-49357

Sequence 49357, Application US/09270767

GENERAL INFORMATION:

APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*

FILE REFERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 49357

LENGTH: 103

TYPE: PRT

ORGANISM: *Drosophila melanogaster*

US-09-270-767-49357

Query Match

Best Local Similarity 100.0%; Score 43; DB 16; Length 103;  
Pred. No. 1.9e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCGKTC 6

Db 87 CCGKTC 92

RESULT 4

US-09-270-849B-180217

Sequence 180217, Application US/09270849B

GENERAL INFORMATION:

APPLICANT: Swimmer et al.

TITLE OF INVENTION: Insect genome survey devices

FILE REFERENCE:

CURRENT APPLICATION NUMBER: US/09/270,849B

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 195450

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 180217

LENGTH: 103

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Synthetic

US-09-270-849B-180217

Query Match  
Best Local Similarity 100.0%; Score 43; DB 16; Length 103;  
Pred. No. 1.9e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCGKTC 6

Db 87 CCGKTC 92

RESULT 5

US-09-688-052-3216

Sequence 3216, Application US/09688052

GENERAL INFORMATION:

APPLICANT: ALEXANDROV, Nikolai

APPLICANT: BROVER, Vyacheslav

TITLE OF INVENTION: Sequence-determined DNA Fragments and Corresponding Polypeptide

TITLE OF INVENTION: Thereby

FILE REFERENCE: 2750-1238P

CURRENT APPLICATION NUMBER: US/09/688,052

CURRENT FILING DATE: 2000-10-13

NUMBER OF SEQ ID NOS: 4086

SEQ ID NO 3216

LENGTH: 121

TYPE: PRT

ORGANISM: *Arabidopsis thaliana*

FEATURE:

NAME/KEY: misc.feature

LOCATION: 1..121

OTHER INFORMATION: Xaa is any amino acid

NAME/KEY: misc.feature

LOCATION: 1..121

OTHER INFORMATION: Ceres Seq. ID 1600282

US-09-688-052-3216

Query Match

Best Local Similarity 90.7%; Score 39; DB 20; Length 121;  
Pred. No. 7.7e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCGKTC 6

Db 94 CCGKTC 99

RESULT 6

US-09-270-767-46709

Sequence 46709, Application US/09270767

GENERAL INFORMATION:

APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*

FILE REFERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 46709

LENGTH: 475

TYPE: PRT

ORGANISM: *Drosophila melanogaster*

US-09-270-767-46709

Query Match

Best Local Similarity 90.7%; Score 39; DB 16; Length 475;  
Pred. No. 2e+03;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCGKTC 6

Db 330 CCGKTC 335

RESULT 7

US-09-270-767-42679

Sequence 42679, Application US/09270767

US-09-270-767-42679



us-09-555-115a-66.rapn

[illegible]

RESULT A 892-269 Application  
269, APPLICATION P.  
US-10-205-892-269  
INFORMATION; Kevin

[illegible]

APPLICANT: ZINTEK - AC1957  
INVENTOR: ZINTEK - AC1957  
APPLICANT INVENTION: P3430R1C57  
TITLE OF INVENTION: P3430R1C57  
PRIORITY NUMBER: 07-26  
PRIORITY DATE: 2002-10/05286

TITLE REFERENCE DATE: 2002-01-15  
FILE APPLICATION NUMBER: 2002-01-60/059263  
CURRENT FILING DATE: 2002-01-18  
CURRENT PUBLICATION DATE: 2002-01-18  
CURRENT APPLICATION NUMBER: 2002-01-60/059266

PRIOR FILING DATE: 1987-09-18  
PRIOR APPLICATION NUMBER: 062250  
PRIOR FILING DATE: 1987-09-18  
PRIOR APPLICATION NUMBER: 063120

Prior Filing Date:  
Prior Application:  
Prior Applicant:  
Prior Filing Date:  
Prior Application:  
Prior Applicant:

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86

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See file

9504

Gaps

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CI 6900X NUMBER: 04-2-  
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DB 1: 1  
1-7e+03: 1; 1

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DATE: 8/23/88  
PAGE: 0  
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NOFID ID: 06504-28  
SOFT: 100  
LENGTH: 100  
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 ANP: Hoffman, Jeff. pet.  
 Hall, L. Ho. Inc.  
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 APPLICANT: Alphonse  
 APPLICANT: Invoice  
 APPLICANT: INVENTION  
 DATE: 1993  
 NOS: 1-07  
 Ver: 2.0

Page 38: Dis  
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APPLICANT'S NAME  
TITLE OF INVENTION  
FILE NO.  
SERIAL NO.  
CLASSIFICATION  
PRIORITY CLAIMS  
ABSTRACT  
DRAWINGS  
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CURRER: 28  
NUMBER: 252  
SOFTWARE: 252  
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8. Mr. Valenzuela, Jeff Peter  
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DB 82 CCGTTC 87

## RESULT 5

US-10-174-575-269  
Sequence 269, Application US/10174575

## GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.  
APPLICANT: Chen, Jian  
APPLICANT: Desnoyers, Luc  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Pan, James  
APPLICANT: Smith, Victoria  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3430R1C35  
CURRENT FILING DATE: 2002-06-18  
PRIOR APPLICATION NUMBER: US/10/174,575  
PRIOR FILING DATE: 2002-01-15  
PRIOR APPLICATION NUMBER: 60/052586  
PRIOR FILING DATE: 1997-09-18  
PRIOR APPLICATION NUMBER: 60/059263  
PRIOR FILING DATE: 1997-09-18  
PRIOR APPLICATION NUMBER: 60/059266  
PRIOR FILING DATE: 1997-09-18  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/063120  
PRIOR FILING DATE: 1997-10-24  
PRIOR APPLICATION NUMBER: 60/063121  
PRIOR FILING DATE: 1997-10-24  
PRIOR APPLICATION NUMBER: 60/063486  
PRIOR FILING DATE: 1997-10-21  
PRIOR APPLICATION NUMBER: 60/063540  
PRIOR FILING DATE: 1997-10-28  
PRIOR APPLICATION NUMBER: 60/063541  
PRIOR FILING DATE: 1997-10-28  
PRIOR APPLICATION NUMBER: 60/063544  
PRIOR FILING DATE: 1997-10-28  
Remaining Prior Application data removed - See file wrapper or PALM.  
NUMBER OF SEQ ID NOS: 612  
SEQ ID NO 269  
LENGTH: 1300  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-10-174-575-269

## Query Match

Best Local Similarity 86.0%; Score 37; DB 6; Length 1300;  
Pred. No. 4.6e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CCGKTC 6  
DB 82 CCGTTC 87

## RESULT 6

US-10-174-575A-269  
Sequence 269, Application US/10174575A

## GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.  
APPLICANT: Chen, Jian  
APPLICANT: Desnoyers, Luc  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Pan, James  
APPLICANT: Smith, Victoria

APPLICANT: Watanabe, Colin K.

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3430R1C35

CURRENT FILING DATE: 2002-06-18

PRIOR APPLICATION NUMBER: US/10/174,575A

PRIOR FILING DATE: 2002-01-15

PRIOR APPLICATION NUMBER: 60/052586

PRIOR FILING DATE: 1997-09-18

PRIOR APPLICATION NUMBER: 60/059263

PRIOR FILING DATE: 1997-09-18

PRIOR APPLICATION NUMBER: 60/059266

PRIOR FILING DATE: 1997-09-18

PRIOR APPLICATION NUMBER: 60/062250

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/063120

PRIOR FILING DATE: 1997-10-24

PRIOR APPLICATION NUMBER: 60/063121

PRIOR FILING DATE: 1997-10-24

PRIOR APPLICATION NUMBER: 60/063486

PRIOR FILING DATE: 1997-10-21

PRIOR APPLICATION NUMBER: 60/063540

PRIOR FILING DATE: 1997-10-28

PRIOR APPLICATION NUMBER: 60/063541

PRIOR FILING DATE: 1997-10-28

PRIOR APPLICATION NUMBER: 60/063544

PRIOR FILING DATE: 1997-10-28

Remaining Prior Application data removed - See file wrapper or PALM.

NUMBER OF SEQ ID NOS: 612

SEQ ID NO 269

LENGTH: 1300

TYPE: PRT

ORGANISM: Homo Sapien

US-10-174-575A-269

OY 1 CCGKTC 6  
DB 82 CCGTTC 87

## Query Match

Best Local Similarity 86.0%; Score 37; DB 6; Length 1300;  
Pred. No. 4.6e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

## RESULT 7

US-10-187-755-269  
Sequence 269, Application US/10187755

## GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.  
APPLICANT: Chen, Jian  
APPLICANT: Desnoyers, Luc  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Pan, James  
APPLICANT: Smith, Victoria  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3430R1C1  
CURRENT FILING DATE: 2002-07-01  
PRIOR APPLICATION NUMBER: US/10/187,755  
PRIOR FILING DATE: 2002-01-15  
PRIOR APPLICATION NUMBER: 60/052586  
PRIOR FILING DATE: 1997-09-18  
PRIOR APPLICATION NUMBER: 60/059263  
PRIOR FILING DATE: 1997-09-18  
PRIOR APPLICATION NUMBER: 60/059266  
PRIOR FILING DATE: 1997-09-18  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17

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;; PRIOR APPLICATION NUMBER: 60/063120
;; PRIOR FILING DATE: 1997-10-24
;; PRIOR APPLICATION NUMBER: 60/063121
;; PRIOR FILING DATE: 1997-10-24
;; PRIOR APPLICATION NUMBER: 60/063486
;; PRIOR FILING DATE: 1997-10-21
;; PRIOR APPLICATION NUMBER: 60/063540
;; PRIOR FILING DATE: 1997-10-28
;; PRIOR APPLICATION NUMBER: 60/063541
;; PRIOR FILING DATE: 1997-10-28
;; PRIOR APPLICATION NUMBER: 60/063544
;; PRIOR FILING DATE: 1997-10-28
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 612
;; SEQ ID NO 269
;; LENGTH: 1300
;; TYPE: PRT
;; ORGANISM: Homo Sapien
US-10-187-755-269

Query Match
Best Local Similarity 86.0%; Score 37; DB 6; Length 1300;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCGKTC 6
DB 82 CCGTTC 87

RESULT 8
US-10-187-749-269
;; Sequence 269, Application US/10187749
;; GENERAL INFORMATION:
;; APPLICANT: Baker, Kevin P.
;; APPLICANT: Chen, Jian
;; APPLICANT: Desnoyers, Luc
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Guiney, Austin L.
;; APPLICANT: Pan, James
;; APPLICANT: Smith, Victoria
;; APPLICANT: Watanabe, Colin K.
;; APPLICANT: Wood, William I.
;; APPLICANT: Zhang, Zemin
;; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;; FILE REFERENCE: P3430R1C1
;; CURRENT APPLICATION NUMBER: US/10/187,749
;; CURRENT FILING DATE: 2002-07-01
;; PRIOR APPLICATION NUMBER: US/10/052,586
;; PRIOR FILING DATE: 2002-01-15
;; PRIOR APPLICATION NUMBER: 60/059263
;; PRIOR FILING DATE: 1997-09-18
;; PRIOR APPLICATION NUMBER: 60/059266
;; PRIOR FILING DATE: 1997-09-18
;; PRIOR APPLICATION NUMBER: 60/062250
;; PRIOR FILING DATE: 1997-10-17
;; PRIOR APPLICATION NUMBER: 60/063120
;; PRIOR FILING DATE: 1997-10-24
;; PRIOR APPLICATION NUMBER: 60/063121
;; PRIOR FILING DATE: 1997-10-24
;; PRIOR APPLICATION NUMBER: 60/063486
;; PRIOR FILING DATE: 1997-10-21
;; PRIOR APPLICATION NUMBER: 60/063540
;; PRIOR FILING DATE: 1997-10-28
;; PRIOR APPLICATION NUMBER: 60/063541
;; PRIOR FILING DATE: 1997-10-28
;; PRIOR APPLICATION NUMBER: 60/063544
;; PRIOR FILING DATE: 1997-10-28
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 612
;; SEQ ID NO 269
;; LENGTH: 1300
;; TYPE: PRT
;; ORGANISM: Homo Sapien
US-10-187-749-269
```

```
;; TYPE: PRT
;; ORGANISM: Homo Sapien
US-10-187-749-269

Query Match
Best Local Similarity 86.0%; Score 37; DB 6; Length 1300;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCGKTC 6
DB 82 CCGTTC 87

RESULT 9
US-10-199-672-269
;; Sequence 269, Application US/10199672
;; GENERAL INFORMATION:
;; APPLICANT: Baker, Kevin P.
;; APPLICANT: Chen, Jian
;; APPLICANT: Desnoyers, Luc
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Guiney, Austin L.
;; APPLICANT: Pan, James
;; APPLICANT: Smith, Victoria
;; APPLICANT: Watanabe, Colin K.
;; APPLICANT: Wood, William I.
;; APPLICANT: Zhang, Zemin
;; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;; FILE REFERENCE: P3430R1C1
;; CURRENT APPLICATION NUMBER: US/10/199,672
;; CURRENT FILING DATE: 2002-07-18
;; PRIOR APPLICATION NUMBER: US/10/052,586
;; PRIOR FILING DATE: 2002-01-15
;; PRIOR APPLICATION NUMBER: 60/059263
;; PRIOR FILING DATE: 1997-09-18
;; PRIOR APPLICATION NUMBER: 60/059266
;; PRIOR FILING DATE: 1997-09-18
;; PRIOR APPLICATION NUMBER: 60/062250
;; PRIOR FILING DATE: 1997-10-17
;; PRIOR APPLICATION NUMBER: 60/063120
;; PRIOR FILING DATE: 1997-10-24
;; PRIOR APPLICATION NUMBER: 60/063121
;; PRIOR FILING DATE: 1997-10-24
;; PRIOR APPLICATION NUMBER: 60/063486
;; PRIOR FILING DATE: 1997-10-21
;; PRIOR APPLICATION NUMBER: 60/063540
;; PRIOR FILING DATE: 1997-10-28
;; PRIOR APPLICATION NUMBER: 60/063541
;; PRIOR FILING DATE: 1997-10-28
;; PRIOR APPLICATION NUMBER: 60/063544
;; PRIOR FILING DATE: 1997-10-28
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 612
;; SEQ ID NO 269
;; LENGTH: 1300
;; TYPE: PRT
;; ORGANISM: Homo Sapien
US-10-199-672-269

Query Match
Best Local Similarity 86.0%; Score 37; DB 6; Length 1300;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCGKTC 6
DB 82 CCGTTC 87

RESULT 10
US-10-194-486-269
;; Sequence 269, Application US/10194486
```

```

: GENERAL INFORMATION:
: APPLICANT: Baker, Kevin P.
: APPLICANT: Chen, Jian
: APPLICANT: Desnoyers, Luc
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Gurney, Austin L.
: APPLICANT: Pan, James
: APPLICANT: Smith, Victoria
: APPLICANT: Watanabe, Colin K.
: APPLICANT: Wood, William I.
: APPLICANT: Zhang, Zemin
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: FILE OF INVENTION: ACIDS ENCODING THE SAME
: FILE REFERENCE: P3430R1C1
: CURRENT FILING DATE: 2002-07-11
: PRIOR APPLICATION NUMBER: US/10/052,586
: PRIOR FILING DATE: 2002-01-15
: PRIOR APPLICATION NUMBER: 60/059263
: PRIOR FILING DATE: 1997-09-18
: PRIOR APPLICATION NUMBER: 60/059266
: PRIOR FILING DATE: 1997-09-18
: PRIOR APPLICATION NUMBER: 60/062250
: PRIOR FILING DATE: 1997-10-17
: PRIOR APPLICATION NUMBER: 60/063120
: PRIOR FILING DATE: 1997-10-24
: PRIOR APPLICATION NUMBER: 60/063121
: PRIOR FILING DATE: 1997-10-24
: PRIOR APPLICATION NUMBER: 60/063486
: PRIOR FILING DATE: 1997-10-21
: PRIOR APPLICATION NUMBER: 60/063540
: PRIOR FILING DATE: 1997-10-28
: PRIOR APPLICATION NUMBER: 60/063541
: PRIOR FILING DATE: 1997-10-28
: PRIOR APPLICATION NUMBER: 60/063544
: PRIOR FILING DATE: 1997-10-28
: Remaining prior Application data removed - See File Wrapper or PALM.
: NUMBER OF SEQ ID NOS: 612
: SEQ ID NO 269
: LENGTH: 1300
: TYPE: PRT
: ORGANISM: Homo Sapien
: US-10-194-486-269

Query Match      86.0%; Score 37; DB 6; Length 1300;
Best Local Similarity 83.3%; Pred. No. 4.6e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY      1 CCGKTC 6
DB      82 CCGTTC 87

RESULT 11
US-10-125-923A-451
: GENERAL INFORMATION:
: APPLICANT: Baker, Kevin P.
: APPLICANT: Chen, Jian
: APPLICANT: Desnoyers, Luc
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Gurney, Austin L.
: APPLICANT: Pan, James
: APPLICANT: Smith, Victoria
: APPLICANT: Watanabe, Colin K.
: APPLICANT: Wood, William I.
: APPLICANT: Zhang, Zemin
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: FILE REFERENCE: P3430R1C79
: CURRENT APPLICATION NUMBER: US/10/125,923A
```

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: CURRENT FILING DATE: 2002-01-15
: PRIOR APPLICATION NUMBER: 10/052586
: PRIOR FILING DATE: 2002-01-15
: PRIOR APPLICATION NUMBER: 60/059263
: PRIOR FILING DATE: 1997-09-18
: PRIOR APPLICATION NUMBER: 60/059266
: PRIOR FILING DATE: 1997-09-18
: PRIOR APPLICATION NUMBER: 60/062250
: PRIOR FILING DATE: 1997-10-17
: PRIOR APPLICATION NUMBER: 60/063120
: PRIOR FILING DATE: 1997-10-24
: PRIOR APPLICATION NUMBER: 60/063121
: PRIOR FILING DATE: 1997-10-24
: PRIOR APPLICATION NUMBER: 60/063540
: PRIOR FILING DATE: 1997-10-28
: PRIOR APPLICATION NUMBER: 60/063541
: PRIOR FILING DATE: 1997-10-28
: PRIOR APPLICATION NUMBER: 60/063544
: PRIOR FILING DATE: 1997-10-28
: Remaining prior Application data removed - See File Wrapper or PALM.
: NUMBER OF SEQ ID NOS: 612
: SEQ ID NO 451
: LENGTH: 1743
: TYPE: PRT
: ORGANISM: Homo Sapien
: US-10-125-923A-451

Query Match      86.0%; Score 37; DB 6; Length 1743;
Best Local Similarity 83.3%; Pred. No. 5.7e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY      1 CCGKTC 6
DB      1187 CCGATC 1192

RESULT 12
US-10-205-892-451
: GENERAL INFORMATION:
: APPLICANT: Baker, Kevin P.
: APPLICANT: Chen, Jian
: APPLICANT: Desnoyers, Luc
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Gurney, Austin L.
: APPLICANT: Pan, James
: APPLICANT: Smith, Victoria
: APPLICANT: Watanabe, Colin K.
: APPLICANT: Wood, William I.
: APPLICANT: Zhang, Zemin
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: FILE OF INVENTION: ACIDS ENCODING THE SAME
: FILE REFERENCE: P3430R1C517
: CURRENT APPLICATION NUMBER: US/10/205,892
: CURRENT FILING DATE: 2002-07-26
: PRIOR APPLICATION NUMBER: 10/052586
: PRIOR FILING DATE: 2002-01-15
: PRIOR APPLICATION NUMBER: 60/059263
: PRIOR FILING DATE: 1997-09-18
: PRIOR APPLICATION NUMBER: 60/059266
: PRIOR FILING DATE: 1997-09-18
: PRIOR APPLICATION NUMBER: 60/062250
: PRIOR FILING DATE: 1997-10-17
: PRIOR APPLICATION NUMBER: 60/063120
: PRIOR FILING DATE: 1997-10-24
: PRIOR APPLICATION NUMBER: 60/063121
: PRIOR FILING DATE: 1997-10-24
: PRIOR APPLICATION NUMBER: 60/063486
: PRIOR FILING DATE: 1997-10-21
: PRIOR APPLICATION NUMBER: 60/063540
```

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: PRIOR FILING DATE: 1997-10-28
: PRIOR APPLICATION NUMBER: 60/063541
: PRIOR FILING DATE: 1997-10-28
: PRIOR APPLICATION NUMBER: 60/063544
: PRIOR FILING DATE: 1997-10-28
: Remaining Prior Application data removed - See File Wrapper or PALM.
: NUMBER OF SEQ ID NOS: 612
: SEQ ID NO 451
: LENGTH: 1743
: TYPE: PRT
: ORGANISM: Homo Sapien
US-10-205-892-451

Query Match
Best Local Similarity 86.0%; Score 37; DB 6; Length 1743;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 CCGKTC 6
Db 1187 CCGATC 1192

RESULT 13
US-10-174-575-451
: Sequence 451, Application US/10174575
: GENERAL INFORMATION:
: APPLICANT: Baker, Kevin P.
: APPLICANT: Chen, Jian
: APPLICANT: Desnoyers, Luc
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Gurney, Austin L.
: APPLICANT: Pan, James
: APPLICANT: Smith, Victoria
: APPLICANT: Watanabe, Colin K.
: APPLICANT: Wood, William I.
: APPLICANT: Zhang, Zemin
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: TITLE OF INVENTION: ACIDS ENCODING THE SAME
: FILE REFERENCE: P3430R1C35
: CURRENT APPLICATION NUMBER: US/10/174,575
: CURRENT FILING DATE: 2002-06-18
: PRIOR APPLICATION NUMBER: 10/052586
: PRIOR FILING DATE: 2002-01-15
: PRIOR APPLICATION NUMBER: 60/059263
: PRIOR FILING DATE: 1997-09-18
: PRIOR APPLICATION NUMBER: 60/059266
: PRIOR FILING DATE: 1997-09-18
: PRIOR APPLICATION NUMBER: 60/062250
: PRIOR FILING DATE: 1997-10-17
: PRIOR APPLICATION NUMBER: 60/063120
: PRIOR FILING DATE: 1997-10-24
: PRIOR APPLICATION NUMBER: 60/063121
: PRIOR FILING DATE: 1997-10-24
: PRIOR APPLICATION NUMBER: 60/063486
: PRIOR FILING DATE: 1997-10-21
: PRIOR APPLICATION NUMBER: 60/063540
: PRIOR FILING DATE: 1997-10-28
: PRIOR APPLICATION NUMBER: 60/063541
: PRIOR FILING DATE: 1997-10-28
: PRIOR APPLICATION NUMBER: 60/063544
: PRIOR FILING DATE: 1997-10-28
: Remaining Prior Application data removed - See File Wrapper or PALM.
: NUMBER OF SEQ ID NOS: 612
: SEQ ID NO 451
: LENGTH: 1743
: TYPE: PRT
: ORGANISM: Homo Sapien
US-10-174-575-451

Query Match
Best Local Similarity 86.0%; Score 37; DB 6; Length 1743;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

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Oy 1 CCGKTC 6
Db 1187 CCGATC 1192

RESULT 14
US-10-174-575A-451
: Sequence 451, Application US/10174575A
: GENERAL INFORMATION:
: APPLICANT: Baker, Kevin P.
: APPLICANT: Chen, Jian
: APPLICANT: Desnoyers, Luc
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Gurney, Austin L.
: APPLICANT: Pan, James
: APPLICANT: Smith, Victoria
: APPLICANT: Watanabe, Colin K.
: APPLICANT: Wood, William I.
: APPLICANT: Zhang, Zemin
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: TITLE OF INVENTION: ACIDS ENCODING THE SAME
: FILE REFERENCE: P3430R1C35
: CURRENT APPLICATION NUMBER: US/10/174,575A
: CURRENT FILING DATE: 2002-06-18
: PRIOR APPLICATION NUMBER: 10/052586
: PRIOR FILING DATE: 2002-01-15
: PRIOR APPLICATION NUMBER: 60/059263
: PRIOR FILING DATE: 1997-09-18
: PRIOR APPLICATION NUMBER: 60/059266
: PRIOR FILING DATE: 1997-09-18
: PRIOR APPLICATION NUMBER: 60/062250
: PRIOR FILING DATE: 1997-10-17
: PRIOR APPLICATION NUMBER: 60/063120
: PRIOR FILING DATE: 1997-10-24
: PRIOR APPLICATION NUMBER: 60/063121
: PRIOR FILING DATE: 1997-10-24
: PRIOR APPLICATION NUMBER: 60/063486
: PRIOR FILING DATE: 1997-10-21
: PRIOR APPLICATION NUMBER: 60/063540
: PRIOR FILING DATE: 1997-10-28
: PRIOR APPLICATION NUMBER: 60/063541
: PRIOR FILING DATE: 1997-10-28
: PRIOR APPLICATION NUMBER: 60/063544
: PRIOR FILING DATE: 1997-10-28
: Remaining Prior Application data removed - See File Wrapper or PALM.
: NUMBER OF SEQ ID NOS: 612
: SEQ ID NO 451
: LENGTH: 1743
: TYPE: PRT
: ORGANISM: Homo Sapien
US-10-174-575A-451

Query Match
Best Local Similarity 86.0%; Score 37; DB 6; Length 1743;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 CCGKTC 6
Db 1187 CCGATC 1192

RESULT 15
US-10-187-755-451
: Sequence 451, Application US/10187755
: GENERAL INFORMATION:
: APPLICANT: Baker, Kevin P.
: APPLICANT: Chen, Jian
: APPLICANT: Desnoyers, Luc
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Gurney, Austin L.
```



APPLICANT: Pan,James  
APPLICANT: Smith,Victoria  
APPLICANT: Watanabe,Colin K.  
APPLICANT: Wood,William I.  
APPLICANT: Zhang,Zemin  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE OF INVENTION: ACIDS ENCODING THE SAME  
FILE REFERENCE: P3430R1C1  
CURRENT APPLICATION NUMBER: US/10/187,755  
CURRENT FILING DATE: 2002-07-01  
PRIOR APPLICATION NUMBER: US/10/052,586  
PRIOR FILING DATE: 2002-01-15  
PRIOR APPLICATION NUMBER: 60/059263  
PRIOR FILING DATE: 1997-09-18  
PRIOR APPLICATION NUMBER: 60/059266  
PRIOR FILING DATE: 1997-09-18  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/063120  
PRIOR FILING DATE: 1997-10-24  
PRIOR APPLICATION NUMBER: 60/063121  
PRIOR FILING DATE: 1997-10-24  
PRIOR APPLICATION NUMBER: 60/063486  
PRIOR FILING DATE: 1997-10-21  
PRIOR APPLICATION NUMBER: 60/063540  
PRIOR FILING DATE: 1997-10-28  
PRIOR APPLICATION NUMBER: 60/063541  
PRIOR FILING DATE: 1997-10-28  
PRIOR APPLICATION NUMBER: 60/063544  
PRIOR FILING DATE: 1997-10-28  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 612  
SEQ ID NO 451  
LENGTH: 1743  
TYPE: PRT  
ORGANISM: Homo Saplen  
US-10-187-755-451

Query Match 86.0%; Score 37; DB 6; Length 1743;  
Best Local Similarity 83.3%; Pred. No. 5.7e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CCGKTC 6  
11111  
Db 1187 CCGATC 1192

Search completed: May 6, 2003, 10:36:15  
Job time : 87 secs

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